

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: July 15, 2003, 07:15:55 ; Search time 41 Seconds
(without alignments)
801.902 Million cell updates/sec

Title: US-09-940-063-2
Perfect score: 1794
Sequence: 1 MAEHYHEDYGFSSFNDSQ.....DNKTFSSHVTEATSMFQL 342

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Reached: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.73.*
2: PIR1.*
3: PIR2.*
4: PIR3.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	619	34.5	369	2	JC5068
2	608.5	33.9	378	2	B55735
3	608.5	33.9	378	2	A55735
4	588.5	32.8	378	2	A45680
5	568	31.7	350	2	JN0621
6	524.5	29.2	352	2	A45747
7	521.5	29.1	374	2	I38450
8	520.5	29.0	360	2	JC2443
9	516	28.8	353	2	S28787
10	512.5	28.6	355	2	A45177
11	508.5	28.3	352	2	G00048
12	508	28.3	359	2	A48921
13	507.5	28.3	358	2	A53752
14	505.5	28.2	360	2	A57160
15	505	28.1	355	2	J01231
16	498.5	27.8	359	2	I49341
17	497.5	27.7	367	2	J50349
18	495.5	27.6	355	2	G02436
19	494	27.5	352	2	A43113
20	491.5	27.4	383	2	S55594
21	490	27.3	360	2	S55611
22	489	27.3	360	2	UC4587
23	484	27.0	356	2	S42096
24	484	27.0	359	2	S15403
25	481	26.8	359	2	JC1104
26	478	26.6	359	2	A48857
27	477	26.6	359	2	S44425
28	476.5	26.6	350	2	A39445
29	476.5	26.6	355	2	I49339

30	474	26.4	359	2	A42656	angiotensin II rec
31	469	26.1	356	2	I49340	MRP-1 alpha recept
32	467	26.0	359	2	JC2134	angiotensin II rec
33	465.5	25.9	355	2	JC5067	G protein-coupled
34	465	25.9	359	2	I39418	angiotensin II rec
35	465	25.9	359	2	JH0621	angiotensin II rec
36	458	25.5	359	2	JC1194	angiotensin II rec
37	458	25.5	359	2	J01516	angiotensin II rec
38	447	24.9	355	2	JC4304	orphan G protein-c
39	444	24.7	374	2	S32785	G protein-coupled
40	442	24.6	359	2	I51372	angiotensin II rec
41	439.5	24.5	354	2	I58186	probable G protein
42	429	23.9	372	2	S26667	G protein-coupled
43	427.5	23.8	354	2	A23669	interleukin-8 rece
44	426.5	23.8	374	2	S42628	G protein-coupled
45	426	23.7	327	2	S56162	MDR1s protein - h

ALIGNMENTS

RESULT 1

JC5068	G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)	
C:Date: 31-Jan-1997	#sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068	
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.	
Biochem. Biophys. Res. Commun. 227, 846-853, 1996	
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-11k	
A:Reference number: JC5067; MUID:97040707; PMID:886020	
A:Accession: JC5068	
A:Molecule type: DNA	
A:Residues: 1-369 <ZAB>	
A:Cross-references: EMBL:Z79784; NID:91668737; PIDN:CA802144.1; PID:91668738	
C:Comment: This protein belongs to the family of alpha chemokine receptors.	
C:Genetics:	
A:Gene: GDB:CMKR6; STRL22; GPR29; CKR6; CKR-L3; GPR-CY4	
A:Cross-references: GDB:5370639; OMIM:601835	
A:Map position: 6q27-6q27	
C:Superfamily: vertebrate rhodopsin	
C:Keywords: G protein-coupled receptor; transmembrane protein	
F:42-68/Domain: transmembrane #status predicted <TM1>	
F:79-99/Domain: transmembrane #status predicted <TM2>	
F:115-136/Domain: transmembrane #status predicted <TM3>	
F:160-180/Domain: transmembrane #status predicted <TM4>	
F:212-233/Domain: transmembrane #status predicted <TM5>	
F:250-271/Domain: transmembrane #status predicted <TM6>	
F:292-315/Domain: transmembrane #status predicted <TM7>	
Query Match	34.5% Score 619; DB 2; Length 369;
Best local similarity	36.3% Pred. No. 1.3e-42; Indels 44; Gaps 9;
Matches 135; Conservative 77; Mismatches 116;	
QY 5 DYHEDYGFSSFNDSOEHDPL-----QFSKVPICMYLVFVCGLSLVIVIS 56	
DB 8 DSSDDY-FVSVNTSVYSVDSSEMLCSLQEVNQFRLPFLAIVSLICVFGILGNLVITF 66	
QY 57 IFYHKLQSLDVEFLVNLPLADLVVVCILPFAVA-GIHEWFGCMCKSLGITTYFT 115	
DB 67 AFYKRSMTDVIYLLNMAIDILFVLTPFAVSHAGCAWVESNATCKLGIYAINEFC 126	
QY 116 SMLITCTIVDRFLVAVKATFAYNOAKRMWGVTSLIIVISLVSIPQIIVGNFL 175	
DB 127 GMLITCTISMDRYIAVOATSFRLRSITICILVWGLSVIISSTFVFNOKYNT 186	
QY 176 D-KLIGYHDEAIS-----TVLATQMTLGFPLPLTMIVCYSVIITLLHAGFOK 228	
DB 187 QGSDVCEPKYQTVSEPIRMKLMGLGELLFEPFLPMFCYFIVKTLVQAQNSRHK 246	
QY 229 SKIIFLVMAVFLTQMFNFM-----KFLRSHWEYVAMTSRHYITMVEALAYL 279	
DB 247 AIRVIAVIVLFLACQIPHNVLVLTATANLGNMRSQSE---KLIGYKTVVEVLAFL 302	

QY 280 RACINPVYIAYVSLKFRNKLVKIDICLPYLGVSQWMS-----SEDSKTSQA 330
DB 303 HCCINPVYIAYIGOKFRNFKILKIDMC-----VRRYKSSGFCAGRYSENISRQTS 357
QY 331 SHNVEATSMFOL 342
DB 358 TADNDNASSFTW 369

RESULT 2

B55735

Lymphocyte-specific G protein-coupled receptor EB11 - human

N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C:Species: Homo sapiens (man)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000

C:Accession: B55735; S52443

R:Schweickart, V.L.; Raport, C.J.; Godtska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: B55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:J31581; NID:q468319; PIDN:AAA74231.1; PID:q468320

R:Burgstahler, R.; Kempkes, B.; Staude, K.; Lipp, M.

Submitted to the EMBL Data Library, February 1995.

A:Description: The expression of the chemokine receptor BUR2/EB11 is specifically trans

A:Reference number: S52443

A:Accession: S52443

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 21-378 <BUR>

A:Cross-references: EMBL:X84702

C:Genetics:

A:Gene: GDB:CMKBR7; EB11; BUR2; CCR7

A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 33.9%; Score 608.5; DB 2; Length 378;

Best Local Similarity 36.9%; Pred. No. 9.1e-42;

Matches 122; Conservative 84; Mismatches 106; Indels 19; Gaps 8;

QY 24 QDLQFSKVLPCMYLVVFCGLVNSLVISIFYHKLQSLDVFVNLPLADLVFVCT 83
DB 51 KDVNFKAMFLPIMYSIICFVGLGNGLVVLYIFKRLKMTDTYLLNLAVADILFLT 110
DB 84 LPFWAYAGIHFWVGVGWCKSLGITYINFTSMILICTIVDRFIYVVKATKAYNOQAK 143
DB 111 LPFWAYSAKSWFVGWGFCKIFAIYKMSFSGMLLCTISIDRYVAIVQVASHRRAR 170
QY 144 RMTGKVTSLIWIWISLVSLPQIYGNV---FNLDKLICY---HDEAISTVVLATQMT 197
DB 171 VLISKISCGIWLAVLSIPELLYSDLRSSSQAMRCSLIEHFAFTTIOYA-QMV 229
QY 198 LGFLLPLMTIMVCSYVILKTLAAGGFQKHSRLKIIFLVMAVFLTLQMPN-----LM 250
DB 230 IGFVLPPLAMSFYLIIRTLQARNFERNKAKIVIAVVVFIVFQLPYNGVLAQTVA 289
QY 251 KF-IRSTHWEYKMTSFHYITMTVEALAYLRACINPVYIAYVSLKFRNKLVKIDIGCL 309
DB 290 NFNTSTSTCSELKQNLNAYD--VYISLACVRCVNPFLYAFIGVFRNDLEKLEKDGCL 347
QY 310 PYLGVSQWMSSEDSKTSFASHNVEATSMF 340
DB 348 SQEOL-RQWSSCR-HIRSSMSVAETTTTF 376

RESULT 3

A55735

G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godtska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled recep

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: A55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:J31580; NID:q468340; PIDN:AAA74232.1; PID:q468341

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 33.9%; Score 608.5; DB 2; Length 378;

Best Local Similarity 36.3%; Pred. No. 9.1e-42;

Matches 120; Conservative 84; Mismatches 108; Indels 19; Gaps 8;

QY 24 QDLQFSKVLPCMYLVVFCGLVNSLVISIFYHKLQSLDVFVNLPLADLVFVCT 83
DB 51 KDVNFKAMFLPIMYSIICFVGLGNGLVVLYIFKRLKMTDTYLLNLAVADILFLI 110
QY 84 LPFWAYAGIHFWVGVGWCKSLGITYINFTSMILICTIVDRFIYVVKATKAYNOQAK 143
DB 111 LPFWAYSAKSWFVGWGFCKIFAIYKMSFSGMLLCTISIDRYVAIVQVASHRRAR 170
QY 144 RMTGKVTSLIWIWISLVSLPQIYGNV---FNLDKLICY---HDEAISTVVLATQMT 197
DB 171 VLISKISCGIWLAVLSIPELLYSDLRSSSQAMRCSLIEHFAFTTIOYA-QMV 229
QY 198 LGFLLPLMTIMVCSYVILKTLAAGGFQKHSRLKIIFLVMAVFLTLQMPN-----LM 250
DB 230 IGFVLPPLAMSFYLIIRTLQARNFERNKAKIVIAVVVFIVFQLPYNGVLAQTVA 289
QY 251 KF-IRSTHWEYKMTSFHYITMTVEALAYLRACINPVYIAYVSLKFRNKLVKIDIGCL 309
DB 290 NFNTSTSTCSELKQNLNAYD--VYISLACVRCVNPFLYAFIGVFRNDLEKLEKDGCL 347
QY 310 PYLGVSQWMSSEDSKTSFASHNVEATSMF 340
DB 348 SQEOLRH-WSSCR-HVKNASVMEATTTTF 376

RESULT 4

A45680

G protein-coupled peptide receptor EBI 1 - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C:Accession: A45680

R:Bitenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E. J. Virol. 67, 2209-2220, 1993

A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple

A:Reference number: A45680; MUID:93186173; PMID:8383238

A:Accession: A45680

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-378 <BIR>

A:Cross-references: GB:L08176; NID:q183484; PID:q183485

A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIIP:127095)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 32.8%; Score 588.5; DB 2; Length 378;

Best Local Similarity 36.3%; Pred. No. 3.7e-40;

Matches 120; Conservative 84; Mismatches 108; Indels 19; Gaps 8;

QY 24 QDLQFSKVLPCMYLVVFCGLVNSLVISIFYHKLQSLDVFVNLPLADLVFVCT 83
DB 51 KDVNFKAMFLPIMYSIICFVGLGNGLVVLYIFKRLKMTDTYLLNLAVADILFLT 110

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OM protein - protein search, using sw model

Run on: July 15, 2003, 07:02:50 ; Search time 23 seconds

(without alignments)
616.735 Million cell updates/sec

Title: US-09-940-063-2
Perfect score: 1794
Sequence: 1 MAEHYHEDYGFSSFNDSQ.....DNKTFASHNEATSMFQL 342

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 112892
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1794	100.0	342	1 CCR6_HUMAN	O00574 homo sapien
2	1730	96.4	342	1 CCR6_MACNE	O19024 macaca neme
3	1717	95.7	342	1 CCR6_CERAE	O18963 cercopithec
4	1702.5	94.9	343	1 CCR6_MACMU	Q9xt45 macaca mula
5	619	34.5	374	1 CCR6_HUMAN	P16864 homo sapien
6	612	34.1	357	1 CCR6_HUMAN	P16864 homo sapien
7	608.5	33.9	378	1 CCR7_HUMAN	P22248 homo sapien
8	608.5	33.9	378	1 CCR7_HUMAN	P22248 homo sapien
9	608	33.9	369	1 CCR9_MOUSE	P47774 mus musculu
10	598.5	33.4	369	1 CCR9_MOUSE	Q54689 mus musculu
11	568	31.7	350	1 CCR6_BOVIN	P53530 bos taurus
12	560	31.2	350	1 CCR6_HUMAN	Q9np89 homo sapien
13	524.5	29.2	352	1 CCR4_HUMAN	P10991 homo sapien
14	524	29.2	353	1 CCR4_FELCA	P56498 felis silve
15	521.5	29.1	349	1 CCR4_RAT	O08565 rattus norv
16	521.5	29.1	360	1 CCR2_MACMU	O18793 macaca mula
17	521.5	29.1	374	1 CCR2_HUMAN	P15997 homo sapien
18	516	28.8	353	1 CCR4_BOVIN	P55930 bos taurus
19	515.5	28.7	352	1 CCR4_PAPAN	P56491 papio anubi
20	514.5	28.6	352	1 CCR4_MACMU	P79334 macaca mula
21	512.5	28.6	355	1 CCR1_HUMAN	P12246 homo sapien
22	511.5	28.5	352	1 CCR4_CERTO	O62747 cercocobus
23	510	28.4	359	1 CCR4_MOUSE	P70658 m.c-x-c che
24	509	28.4	373	1 CCR2_RAT	O55193 rattus norv
25	508.5	28.3	352	1 CCR4_MACPA	Q28474 macaca fasc
26	508.5	28.3	354	1 CCR5_RAT	O08556 rattus norv
27	508	28.3	359	1 IL8B_MOUSE	P53343 mus musculu
28	508	28.3	373	1 CCR2_MOUSE	P16863 mus musculu
29	507.5	28.3	358	1 IL8B_RABIT	P53344 oryctolagus
30	505.5	28.2	360	1 CCR4_HUMAN	P1679 homo sapien
31	505	28.1	355	1 IL8A_RABIT	P21109 oryctolagus
32	503.5	28.1	356	1 IL8B_CANFA	O97571 canis fami
33	502	28.0	368	1 CCR3_HUMAN	P49682 homo sapien

34	500	27.9	359	1 CCR3_RAT	O54814 rattus norv
35	499.5	27.8	355	1 CCR3_CERAE	P56492 cercopithec
36	498.5	27.8	355	1 CCR3_HUMAN	P51677 homo sapien
37	497.5	27.7	367	1 CCR3_MOUSE	O88410 mus musculu
38	497	27.7	352	1 CCR5_CERAE	P56493 cercopithec
39	496	27.6	352	1 CCR5_HYLL	O97883 hylobates l
40	495.5	27.6	355	1 CCR3_MACMU	P56483 macaca mula
41	494	27.5	352	1 CCR5_GORGO	P56439 gorilla gor
42	494	27.5	352	1 CCR5_HUMAN	P51681 homo sapien
43	493.5	27.5	352	1 CCR3_MOUSE	P51678 mus musculu
44	493	27.5	352	1 CCR5_TRAFR	O97878 trachypithe
45	492.5	27.5	358	1 CCR3_CAVVO	Q92213 cavia porce

ALIGNMENTS

```

RESULT 1
ID CCR6_HUMAN STANDARD: PRT: 342 AA.
AC O00574: 000575:
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled
DE receptor bonzo) (G protein-coupled receptor STRL33).
GN CXCR6 OR BONZO OR STRL33 OR TYMSR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., KewalRamani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RT immunodeficiency viruses."
RL Nature 388:296-300(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97311099; PubMed=9166430;
RA Lao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A.,
RA Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic
RT HIV-1."
RL J. Exp. Med. 185:2015-2023(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97431687; PubMed=9285716;
RA Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
RA Loetscher P., Arenzana-Seisdedos F., Moser B.;
RT "TYMSR, a putative chemokine receptor selectively expressed in
RT activated T cells, exhibits HIV-1 coreceptor function."
RL Curr. Biol. 7:652-660(1997).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
CC CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T
CC CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to: license@isb-sib.ch).
CC -----
CC EMBL: AF007545; AAB64221.1; -

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DR EMBL: U73529; AAB61456.1; -
 DR EMBL: U73531; AAB61457.1; -
 DR EMBL: Y13248; CAA73698.1; -
 DR MIM: 605163; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECIP_F1.1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECIP_F1.2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 FT DOMAIN 1 32
 FT TRANSSEM 33 59
 FT DOMAIN 60 68
 FT TRANSSEM 69 89
 FT DOMAIN 90 103
 FT TRANSSEM 104 125
 FT DOMAIN 126 143
 FT TRANSSEM 144 164
 FT DOMAIN 165 187
 FT TRANSSEM 188 215
 FT DOMAIN 216 231
 FT TRANSSEM 232 259
 FT DOMAIN 260 275
 FT TRANSSEM 276 293
 FT DOMAIN 294 342
 FT DISULFID 102 180
 FT CARBOHYD 16 16
 FT VARIANT 25 25
 FT
 SQ SEQUENCE 342 AA; 39280 MM; 9FBC02556D1082E CRC64;
 Query Match 100.0%; Score 1794; DB 1; Length 342;
 Best Local Similarity 100.0%; Pred. No. 8.1e-95;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHYEDYGFSSFNSSOEHDLOFQSKVFLPCMYLVFVCGVGNLSLVYISFYH 60
 DB 1 MAEHYEDYGFSSFNSSOEHDLOFQSKVFLPCMYLVFVCGVGNLSLVYISFYH 60
 QY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQWCKSLGITYINFTSMIL 120
 DB 61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQWCKSLGITYINFTSMIL 120
 QY 121 TCITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIISLVSPQITIGVNFMDLILC 180
 DB 121 TCITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIISLVSPQITIGVNFMDLILC 180
 QY 181 GYHDEAISTVLAQTMTLGFLLPLTMTVCSYVITKILLAGGFQKRSKIIIFLVAVF 240
 DB 181 GYHDEAISTVLAQTMTLGFLLPLTMTVCSYVITKILLAGGFQKRSKIIIFLVAVF 240
 QY 241 LTQMPENLKKFIRSTHWEYVAMTSFHYITMVEALAYLRACINPVLVAFVSLKFRKNF 300
 DB 241 LTQMPENLKKFIRSTHWEYVAMTSFHYITMVEALAYLRACINPVLVAFVSLKFRKNF 300
 QY 301 KLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNEATSMFQL 342
 DB 301 KLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNEATSMFQL 342

RESULT 2
 CCR6_MACNE
 ID CCR6_MACNE STANDARD; PRT; 342 AA.
 AC 019024;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled receptor bonzo).
 DE CXCR6 OR BONZO.
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97373958; PubMed=9230441;
 RA Deng H.K., Unutmaz D., Kewallramani V.N., Littman D.R.;
 RT "Expression cloning of new receptors used by simian and human
 RT Immunodeficiency viruses";
 RL Nature 388:296-300(1997).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
 CC CORECEPTOR BY STVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL: AF007858; AAB64224.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECIP_F1.1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECIP_F1.2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32
 FT TRANSSEM 33 59
 FT DOMAIN 60 68
 FT TRANSSEM 69 89
 FT DOMAIN 90 103
 FT TRANSSEM 104 125
 FT DOMAIN 126 143
 FT TRANSSEM 144 164
 FT DOMAIN 165 187
 FT TRANSSEM 188 215
 FT DOMAIN 216 231
 FT TRANSSEM 232 259
 FT DOMAIN 260 275
 FT TRANSSEM 276 293
 FT DOMAIN 294 342
 FT DISULFID 102 180
 FT CARBOHYD 16 16
 FT
 SQ SEQUENCE 342 AA; 39297 MM; 55F9F68CB62D2D5 CRC64;
 Query Match 96.4%; Score 1730; DB 1; Length 342;
 Best Local Similarity 95.6%; Pred. No. 3.2e-91;
 Matches 327; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAEHYEDYGFSSFNSSOEHDLOFQSKVFLPCMYLVFVCGVGNLSLVYISFYH 60
 DB 1 MAEHYEDYGFSSFNSSOEHDLOFQSKVFLPCMYLVFVCGVGNLSLVYISFYH 60
 QY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQWCKSLGITYINFTSMIL 120
 DB 61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGQWCKSLGITYINFTSMIL 120
 QY 121 TCITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIISLVSPQITIGVNFMDLILC 180
 DB 121 TCITVDFEIVVAKATKAYNOQAKRMWGKYSLLIWIISLVSPQITIGVNFMDLILC 180
 QY 181 GYHDEAISTVLAQTMTLGFLLPLTMTVCSYVITKILLAGGFQKRSKIIIFLVAVF 240
 DB 181 GYHDEAISTVLAQTMTLGFLLPLTMTVCSYVITKILLAGGFQKRSKIIIFLVAVF 240
 QY 241 LTQMPENLKKFIRSTHWEYVAMTSFHYITMVEALAYLRACINPVLVAFVSLKFRKNF 300
 DB 241 LTQMPENLKKFIRSTHWEYVAMTSFHYITMVEALAYLRACINPVLVAFVSLKFRKNF 300
 QY 301 KLVKDIGCLPYLGVSHQWKSSEDSKTFSSASHNEATSMFQL 342

```

Db      301 KLVADICGLPYLGVSQWKKSEDSKTFSSASHNEATSMFOL 342

RESULT 3
CCRB_CERAE      STANDARD:      PRT:      342 AA.
AC      018983;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled
DE      receptor bonzo).
DE      CXCR6 OR BONZO.
OS      Cercopithecus aethiops (Green monkey) (Grivet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecoidea; Cercopithecus.
NCBI_TaxID=9534;
[1]

SEQUENCE FROM N.A.
MEDLINE=97373958; PubMed=9230441;
RA      Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT      "Expression cloning of new receptors used by simian and human
RT      immunodeficiency viruses.";
RL      Nature 388:296-300(1997).
CC      -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
CC      CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF007859; AAB64225.1;
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCR_Rhodopsn.
DR      PROSITE; PS00237; G-PROTEIN_RECPEP_FL_1; 1.
DR      PROSITE; PS50262; G-PROTEIN_RECPEP_FL_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
CC      -----
FT      TRANSMEM      1      32
FT      DOMAIN      33      59
FT      TRANSMEM      60      68
FT      TRANSMEM      69      89
FT      DOMAIN      90      103
FT      TRANSMEM      104      125
FT      TRANSMEM      126      143
FT      TRANSMEM      144      164
FT      TRANSMEM      165      187
FT      TRANSMEM      188      215
FT      TRANSMEM      216      231
FT      TRANSMEM      232      259
FT      TRANSMEM      260      275
FT      TRANSMEM      276      293
FT      DOMAIN      294      342
FT      DISULFID      102      180
FT      CARBOHYD      16
FT      SEQUENCE      342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;

Query Match      95.7%; Score 1717; DB 1; Length 342;
Best Local Similarity 95.3%; Pred. No. 1.7e-90;
Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

```

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Qy      61 KLSLTDFVLNPLADLVEYCYLPENAVAGIHEWFGQVCKSLGIYINFTSMIL 120
Db      61 KLSLTDFVLNPLADLVEYCYLPENAVAGIHEWFGQVCKSLGIYINFTSMIL 120
Qy      121 TCITVDRFIVVVKATKAVNOAKRMWGKYSLLIWIISLVSIPQIITNGVFNLDLILC 180
Db      121 TCITVDRFIVVVKATKAVNOAKRMWGKYSLLIWIISLVSIPQIITNGVFNLDLILC 180
Qy      181 GYHDEAISTVYVLAQMTLGFPLPLTMIVCVSVITIKTLHLHAGGQKRSLSKIFLVMAVF 240
Db      181 GYHDEAISTVYVLAQMTLGFPLPLTMIVCVSVITIKTLHLHAGGQKRSLSKIFLVMAVF 240
Qy      241 LTQTPENLKFIRSTHMEYYAMTSFHYITVTEAIVLACPLNPLVAFVSLKRRNFV 300
Db      241 LTQTPENLKFIRSTHMEYYAMTSFHYITVTEAIVLACPLNPLVAFVSLKRRNFV 300
Qy      301 KLVADICGLPYLGVSQWKKSEDSKTFSSASHNEATSMFOL 342
Db      301 KLVADICGLPYLGVSQWKKSEDSKTFSSASHNEATSMFOL 342

RESULT 4
CCRB_MACMU      STANDARD:      PRT:      343 AA.
AC      09XT45;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      C-X-C chemokine receptor type 6 (CXCR-6) (G protein-coupled
DE      receptor bonzo) (G protein-coupled receptor STRL3).
DE      CXCR6 OR BONZO OR STRL3.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecoidea; Macaca.
NCBI_TaxID=9544;
[1]

SEQUENCE FROM N.A.
MEDLINE=21354176; PubMed=11461684;
RA      Margulies B.J., Hauser D.A., Clements J.E.;
RT      "Identification and comparison of eleven rhesus macaque chemokine
RT      receptors.";
RL      AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC      -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
CC      CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF124380; AAD31419.1;
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCR_Rhodopsn.
DR      PROSITE; PS00237; G-PROTEIN_RECPEP_FL_1; 1.
DR      PROSITE; PS50262; G-PROTEIN_RECPEP_FL_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
CC      -----
FT      TRANSMEM      1      33
FT      DOMAIN      34      60
FT      TRANSMEM      61      69
FT      TRANSMEM      70      90
FT      TRANSMEM      91      104
FT      TRANSMEM      105      126
FT      TRANSMEM      127      144
FT      TRANSMEM      145      165
FT      TRANSMEM      166      188
FT      TRANSMEM      189      216

```


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OM protein - protein search, using sw model

Run on: July 15, 2003, 07:12:35 ; Search time 80 Seconds
(without alignments)
880.851 Million cell updates/sec

Title: US-09-940-063-2

Perfect score: 1794

Sequence: 1 MAEDHYEDGFSSFNDSQ.....DNKTFSSHNEATSMFQL 342

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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1: SPTRMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_oranelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1790	99.8	342	4	O9HCA5
2	1785	99.5	342	6	O9TVI6
3	1692.5	94.3	343	6	O9N0D0
4	1690.5	94.2	343	6	O9BD56
5	1332	74.2	351	11	O9E016
6	1326	73.9	351	11	O9ERH5
7	783	43.6	150	6	O8MNM8
8	771	43.0	149	6	O8MNM7
9	612	34.1	369	4	O9U006
10	605.5	33.8	367	11	O9RIV0
11	584	32.6	368	13	O42444
12	554.5	30.9	350	11	O924I3
13	551.5	30.7	350	11	O8O2M9
14	530.5	29.6	355	6	O9MT08
15	529.5	29.5	347	6	O9M2M4
16	528	29.4	346	6	O9M2M4

17	528	29.4	346	-6	O9M2M3	O9mzn3 nycticebus
18	528	29.4	346	6	O9M2M2	O9mzn2 nycticebus
19	525.5	29.3	347	6	O9M2M0	O9mzn0 alogatta se
20	525.5	29.3	347	6	O9M2M6	O9mzn6 callithec
21	525.5	29.3	353	13	O8QPR5	O8qit5 xenopus lae
22	524.5	29.2	347	6	O9M2M9	O9mzn9 ateles pani
23	523.5	29.2	347	6	O9M2M6	O9mzn6 hylobates c
24	523.5	29.2	347	6	O9M2M5	O9mzn5 hylobates h
25	523.5	29.2	347	6	O9M2M3	O9mzn3 hylobates s
26	523.5	29.2	347	6	O9M2M2	O9mzn2 pongo pygma
27	523.5	29.2	347	6	O9M2M1	O9mzn1 gorilla gor
28	523.5	29.1	352	4	O9M2M5	O9mzn5 pithecia pi
29	522.5	29.1	347	6	O9BXA0	O9bx0 homo sapien
30	521.5	29.1	347	6	O9M2P7	O9mzp7 presbytis s
31	521.5	29.1	347	6	O9M2M8	O9mzn8 callithrix
32	518.5	28.9	347	6	O9M2M7	O9mzn7 callimico g
33	517.5	28.8	349	11	O8V047	O8v047 ratius norv
34	516.5	28.8	347	6	O9M2P6	O9mzp6 presbytis j
35	516.5	28.8	347	6	O9M2P2	O9mzp2 mandrillus
36	516.5	28.8	347	6	O9M2M1	O9mzn1 eulemur mac
37	516	28.8	334	6	O9N1P3	O9n1p3 hylobates l
38	515.5	28.7	347	6	O9M203	O9mz03 pygathrix a
39	515.5	28.7	347	6	O9M2Q2	O9mz02 rhinopithec
40	515.5	28.7	347	6	O9M2Q1	O9mz01 pygathrix b
41	515.5	28.7	347	6	O9M2Q0	O9mz00 pygathrix n
42	515.5	28.7	347	6	O9M2P9	O9mzp9 nasalis lar
43	515.5	28.7	347	6	O9M2P8	O9mzp8 colobus pol
44	515.5	28.7	347	6	O9M2P5	O9mzp5 presbytis p
45	515.5	28.7	347	6	O9M2P4	O9mzp4 presbytis f

ALIGNMENTS

```

RESULT 1
ID O9HCA5 PRELIMINARY; PRT; 342 AA.
AC O9HCA5:
DT 01-MAR-2001 (TREMUREL_16, Created)
DT 01-MAR-2001 (TREMUREL_16, Last sequence update)
DE 01-JUN-2002 (TREMUREL_21, Last annotation update)
DE Mutant G protein-coupled receptor STRL33.
GN STRL33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97311099; PubMed=9166430;
RA Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-
RT 1."
RL J. Exp. Med. 185:2015-2023(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA An P., Winkler C., O'Brien S.J.;
RT "The influence of a STRL33 mutant on the course of HIV-1 infection.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF029759; AAC21918.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; LYMPHOTACTNR.
DR PROSITE: PS00237; G_PROTEIN_RECPT.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39279 MW; CE149633D01D20A CRC64;
Query Match 99.8%; Score 1790; DB 4; Length 342;
Best Local Similarity 99.7%; Pred. No. 4.9e-141;
Matches 341; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```



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QY 1 MAEHDIHEDYGFSSFNDSQOEHDQFLOFSKVFLLPCMYLVFVCGLVGNSLVLVISIFTH 60
DB 1 MAKHDYHEDYGFSSFNDSQOEHDQFLOFSKVFLLPCMYLVFVCGLVGNSLVLVISIFTH 60
QY 61 KLOSLTDFVLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
DB 61 KLOSLTDFVLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
QY 121 TCTITVDFEIVVAKATKAYNOQAKRMWGKTSLLIWIIVISLVSPLQIITGNVFNELDKLIC 180
DB 121 TCTITVDFEIVVAKATKAYNOQAKRMWGKTSLLIWIIVISLVSPLQIITGNVFNELDKLIC 180
QY 181 GYHDEAISTVLAOTMTLGFLLPLLMIVCYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
DB 181 GYHDEAISTVLAOTMTLGFLLPLLMIVCYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALIVLRACLNPVLYAVSLKFRKNF 300
DB 241 LITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALIVLRACLNPVLYAVSLKFRKNF 300
QY 301 KLVKDIGCLPYLGVSQVSHQKSSSEDSKTFSSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSQVSHQKSSSEDSKTFSSASHNVEATSMFOL 342

```

RESULT 2

```

Q9TV16 PRELIMINARY; PRT; 342 AA.
ID 09TV16
AC 09TV16;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE G protein-coupled receptor STRL33.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT gpr15 (Bob).";
RL AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
KW PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;

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Query Match 99.5%; Score 1785; DB 6; Length 342;
Best Local Similarity 99.4%; Pred. No. 1,3e-140;
Matches 340; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAEHDIHEDYGFSSFNDSQOEHDQFLOFSKVFLLPCMYLVFVCGLVGNSLVLVISIFTH 60
DB 1 MAEHDIHEDYGFSSFNDSQOEHDQFLOFSKVFLLPCMYLVFVCGLVGNSLVLVISIFTH 60
QY 61 KLOSLTDFVLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
DB 61 KLOSLTDFVLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
QY 121 TCTITVDFEIVVAKATKAYNOQAKRMWGKTSLLIWIIVISLVSPLQIITGNVFNELDKLIC 180
DB 121 TCTITVDFEIVVAKATKAYNOQAKRMWGKTSLLIWIIVISLVSPLQIITGNVFNELDKLIC 180
QY 181 GYHDEAISTVLAOTMTLGFLLPLLMIVCYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
DB 181 GYHDEAISTVLAOTMTLGFLLPLLMIVCYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240

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DB 181 GYHDEAISTVLAOTMTLGFLLPLLMIVCYSVIITKLLHAGGFQKHSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALIVLRACLNPVLYAVSLKFRKNF 300
DB 241 LITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALIVLRACLNPVLYAVSLKFRKNF 300
QY 301 KLVKDIGCLPYLGVSQVSHQKSSSEDSKTFSSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSQVSHQKSSSEDSKTFSSASHNVEATSMFOL 342

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RESULT 3

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Q9N020 PRELIMINARY; PRT; 343 AA.
ID 09N020
AC 09N020;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE STRL33.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cercopitheciidae; Cercopithecidae.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20261727; Pubmed=10799581;
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
RA Kirchhoff F.;
RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
RT not rhesus macaque STRL33 for efficient entry.";
RL J. Virol. 74:5075-5082(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
RA Kirchhoff F.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237559; AAF68392.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 343 AA; 39589 MW; A75B7A0751C13455 CRC64;

```

```

Query Match 94.3%; Score 1692.5; DB 6; Length 343;
Best Local Similarity 94.5%; Pred. No. 6,2e-133;
Matches 324; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

```

```

QY 1 MAEHDIHEDYGFSSFNDSQOEHDQFLOFSKVFLLPCMYLVFVCGLVGNSLVLVISIFTH 59
DB 1 MAEHDIHEDYGFSSFNDSQOEHDQFLOFSKVFLLPCMYLVFVCGLVGNSLVLVISIFTH 60
QY 60 HKLOSLTDFVLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 119
DB 60 HKLOSLTDFVLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 119
QY 120 LFCITVDFEIVVAKATKAYNOQAKRMWGKTSLLIWIIVISLVSPLQIITGNVFNELDKLIC 179
DB 120 LFCITVDFEIVVAKATKAYNOQAKRMWGKTSLLIWIIVISLVSPLQIITGNVFNELDKLIC 179
QY 181 GYHDEAISTVLAOTMTLGFLLPLLMIVCYSVIITKLLHAGGFQKHSKIIIFLVMAVF 239
DB 181 GYHDEAISTVLAOTMTLGFLLPLLMIVCYSVIITKLLHAGGFQKHSKIIIFLVMAVF 239
QY 240 FLITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALIVLRACLNPVLYAVSLKFRKNF 299
DB 240 FLITOMPENLMKFIKIRSTHWEYAMTSFHYITMVEALIVLRACLNPVLYAVSLKFRKNF 299
QY 300 KLVKDIGCLPYLGVSQVSHQKSSSEDSKTFSSASHNVEATSMFOL 342
DB 300 KLVKDIGCLPYLGVSQVSHQKSSSEDSKTFSSASHNVEATSMFOL 342

```


RESULT 4

Q9BDS6 PRELIMINARY: PRT: 343 AA.
 ID Q9BDS6
 AC Q9BDS6: (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 21, Last annotation update)
 DE Orphan seven transmembrane receptor STRL33.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 NCBI_TaxID=9541;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21134736; PubMed-11242524;
 "Cloning and sequencing of cynomolgus macaque ccr3, gp15, and strl33: potential coreceptors for HIV type 1, HIV type 2, and STV.";
 RL AIDS Res. Hum. Retroviruses 17:371-375(2001).
 DR EMBL, AF291671, AAK25742.1, -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0237; GPCR_RHODOPSN.
 DR PRINTS: PRO1568; LYMPHOTACTNR.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
 DR Receptor; Transmembrane.
 KW SEQUENCE 343 AA; 39472 MW; 0961328F948E7784 CRC64;

Query Match 94.2%; Score 1690.5; DB 6; Length 343;
 Best Local Similarity 94.2%; Pred. No. 9.1e-133;
 Matches 323; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 MAEDHYEDYGF--SSFNDSOEHQDFLQFSKVELPCMYLVVFCGLVNSLVVISIFY 59
 1 MAEDHYEDDGLFNSDSOEHQDFLQFSKVELPCMYLVVFCGLVNSLVVISIFY 60
 DB 1
 QY 60 HKLOSLDVLVNLPLADLVVCTLPFMAVAGIHEWVFGVWCKSLGITYINITYSMI 119
 61 HKLOSLDVLVNLPLADLVVCTLPFMAVAGIHEWVFGVWCKSLGITYINITYSMI 120
 DB 61
 QY 120 LTCITVDFEIVVATKAYNOAKRMVGTSLIWIYSLVSLPOTIYGNVNDKLI 179
 121 LTCITVDFEIVVATKAYNOAKRMVGTSLIWIYSLVSLPOTIYGNVNDKLI 180
 DB 121
 QY 180 CGYHDEAISTVATQMTLGFPLTLMTVICYSVIIRTLHAGGFQKRSKIIFLVAV 239
 181 CGYHDEAISTVATQMTLGFPLTLMTVICYSVIIRTLHAGGFQKRSKIIFLVAV 240
 DB 181
 QY 240 FLITQMPFNLMKFRSTHWEYVAMTSFRHYTMVTEALAYLACINPVLVAVSLKFRNF 299
 241 FLITQMPFNLMKFRSTHWEYVAMTSFRHYTMVTEALAYLACINPVLVAVSLKFRNF 300
 DB 241
 QY 300 WKLVKIDIGCLPYLGVSQWKSSEDSKTFSSASHNVATSMQQL 342
 301 WKLVKIDIGCLPYLGVSQWKSSEDSKTFSSASHNVATSMQQL 343
 DB 301

RESULT 5

Q9E016 PRELIMINARY: PRT: 351 AA.
 ID Q9E016
 AC Q9E016: (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Chemokine receptor CXCR6.
 GN CXCR6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA MacLeodian M., David A., Engel S., Ryan J.E., Cyster J.G.;
 RT "A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo."
 RL Nat. Immunol. 1:298-304(2000).
 DR EMBL, AF301018; AAC34367.1; -
 DR MGI:1934582; Cxcr6.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0237; GPCR_RHODOPSN.
 DR PRINTS: PRO1568; LYMPHOTACTNR.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
 DR Receptor.
 KW SEQUENCE 351 AA; 40468 MW; 5658788372B4C65A CRC64;

Query Match 74.2%; Score 1332; DB 11; Length 351;
 Best Local Similarity 75.2%; Pred. No. 5.8e-103;
 Matches 258; Conservative 36; Mismatches 47; Indels 2; Gaps 1;

QY 2 AEHDYHEDYGFSSFNDS--QEHQDFLQFSKVELPCMYLVVFCGLVNSLVVISIFY 59
 9 ALYDGYEGDEWLFNNSDSQENKRFLEKVEFLPCYLVVFCGLVNSLVVISIFY 68
 DB 9
 QY 60 HKLOSLDVLVNLPLADLVVCTLPFMAVAGIHEWVFGVWCKSLGITYINITYSMI 119
 61 HKLOSLDVLVNLPLADLVVCTLPFMAVAGIHEWVFGVWCKSLGITYINITYSMI 120
 DB 61
 QY 120 LTCITVDFEIVVATKAYNOAKRMVGTSLIWIYSLVSLPOTIYGNVNDKLI 179
 121 LTCITVDFEIVVATKAYNOAKRMVGTSLIWIYSLVSLPOTIYGNVNDKLI 180
 DB 121
 QY 180 CGYHDEAISTVATQMTLGFPLTLMTVICYSVIIRTLHAGGFQKRSKIIFLVAV 239
 181 CGYHDEAISTVATQMTLGFPLTLMTVICYSVIIRTLHAGGFQKRSKIIFLVAV 240
 DB 181
 QY 240 FLITQMPFNLMKFRSTHWEYVAMTSFRHYTMVTEALAYLACINPVLVAVSLKFRNF 299
 241 FLITQMPFNLMKFRSTHWEYVAMTSFRHYTMVTEALAYLACINPVLVAVSLKFRNF 300
 DB 241
 QY 300 WKLVKIDIGCLPYLGVSQWKSSEDSKTFSSASHNVATSMQQL 342
 301 WKLVKIDIGCLPYLGVSQWKSSEDSKTFSSASHNVATSMQQL 351
 DB 301

RESULT 6

Q9ERH5 PRELIMINARY: PRT: 351 AA.
 ID Q9ERH5
 AC Q9ERH5: (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative chemokine receptor.
 GN CXCR6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=SPLEEN;
 RA Sato H., Taniguchi M.;
 RT "Molecular cloning of a putative chemokine receptor preferentially
 expressed in mouse lymphocytes."
 RL submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF305709; AAC31284.1; -
 DR MGI:1934582; Cxcr6.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0237; GPCR_RHODOPSN.

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OM protein - protein search, using sw model

Run on: July 15, 2003, 07:01:55 ; Search time 72 Seconds
(without alignments)
632.940 Million cell updates/sec

Title: US-09-940-063-2
Perfect score: 1794
Sequence: 1 MAEDYHEDYGFSSFNDSQ.....DNKTFSSHNEATSMFQL 342

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSeq_101002.*
2: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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11: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
12: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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14: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
15: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
18: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
19: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSeq2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1794	100.0	342	19 AAW80806	STRL33 protein seq
2	1794	100.0	342	19 AAW54001	Human HEMBL14 prot
3	1794	100.0	342	20 AAT39366	Platelet factor-4
4	1794	100.0	342	20 AAW97783	Human HIV/SIV rece
5	1794	100.0	342	22 AAG80125	Human CXCR6 protei
6	1794	100.0	342	22 AAG79091	Amino acid sequenc
7	1794	100.0	342	22 AAG67239	Amino acid sequenc
8	1794	100.0	342	22 AAU04032	Human HIV transloc
9	1794	100.0	342	22 AAB84422	Amino acid sequenc
10	1730	96.4	342	20 AAW97785	Pig-tailed macaque

11	1730	96.4	342	22 AAU04034
12	1717	95.7	342	20 AAW97784
13	1717	95.7	342	20 AAU04033
14	1332	74.2	351	20 AAT23825
15	1049	58.5	302	19 AAW70001
16	619	34.5	369	22 AAG80113
17	619	34.5	374	22 AAG80112
18	619	34.5	374	23 AAB09291
19	612	34.1	357	21 AAB19605
20	612	34.1	357	21 AAY90615
21	612	34.1	357	22 AAG80117
22	612	34.1	359	22 AAG80116
23	608.5	33.9	358	21 AAR53745
24	608.5	33.9	358	21 AAB21689
25	608.5	33.9	358	23 AAU91231
26	608.5	33.9	378	15 AAR53744
27	608.5	33.9	378	19 AAW48774
28	608.5	33.9	378	21 AAB21688
29	608.5	33.9	378	21 AAB21699
30	608.5	33.9	378	21 AAY90629
31	608.5	33.9	378	22 AAG80114
32	608.5	33.9	378	22 AAB50859
33	608.5	33.9	378	23 AAU91230
34	608.5	33.9	410	15 AAR53743
35	608.5	33.9	410	19 AAW48723
36	608.5	33.9	410	21 AAB21687
37	608.5	33.9	410	21 AAB21687
38	608.5	33.9	410	23 AAU91229
39	608.5	33.9	569	22 AAB61233
40	606	33.8	357	21 AAY90649
41	606	33.8	359	15 AAR53747
42	606	33.8	359	19 AAW48728
43	606	33.8	359	21 AAB21691
44	606	33.8	359	23 AAU91233
45	606	33.8	359	22 AAB56344

ALIGNMENTS

RESULT 1
AAW80806
AAW80806 standard; Protein: 342 AA.

ID	Score	Query Match	Length	DB ID	Description
XX	1794	100.0	342	19 AAW80806	STRL33 protein sequence.
XX	1794	100.0	342	19 AAW54001	Human HEMBL14 prot
XX	1794	100.0	342	20 AAT39366	Platelet factor-4
XX	1794	100.0	342	20 AAW97783	Human HIV/SIV rece
XX	1794	100.0	342	22 AAG80125	Human CXCR6 protei
XX	1794	100.0	342	22 AAG79091	Amino acid sequenc
XX	1794	100.0	342	22 AAG67239	Amino acid sequenc
XX	1794	100.0	342	22 AAU04032	Human HIV transloc
XX	1794	100.0	342	22 AAB84422	Amino acid sequenc
XX	1730	96.4	342	20 AAW97785	Pig-tailed macaque

(USSH) US SEC HEALTH & HUMAN SERVICES.
Alkhatib G, Berger EA, Farber JM, Liao F;
WPI; 1998-557107/47.
N-PSDB; AAW68515.
New isolated fusion accessory factor STRL33 - which mediates HIV
infection of cells, used to develop products for the study,
prevention and therapy of HIV-related disorders

XX Claim 65; Fig 4; 74pp; English.
XX
XX This sequence is the human STRL33 polypeptide that is expressed by
CC the recombinant cell line of the invention. The STRL33 polypeptide is a
CC fusion accessory factor that can function with CD4 to mediate fusion with
CC cells bearing HIV-1 env from both laboratory-adapted TCR-tropic variants
CC and from M-tropic variants. Agents that suppress STRL33 can be used in a
CC method to treat HIV-related disorders. The products and methods can be
CC used for the study, prevention and therapy of HIV-related disorders.
XX
SO Sequence 342 AA:
Query Match 100.0%; Score 1794; DB 19; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.4e-180; Indels 0; Gaps 0;
Matches 342; Conservative 0; Mismatches 0;
QY 1 MAEHDYHEDYGFSSFNDSOEHDQFQSKVFLPCMTLVFVCGVGNLSLVYISIFYH 60
DB 1 MAEHDYHEDYGFSSFNDSOEHDQFQSKVFLPCMTLVFVCGVGNLSLVYISIFYH 60
DB 61 KLSQLTDFVFLNPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
DB 61 KLSQLTDFVFLNPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
QY 121 TCITVDREFIVVKKATKANOAKRMWGKVTSLIWIISLVSLPQITTYGVNFDKILC 180
DB 121 TCITVDREFIVVKKATKANOAKRMWGKVTSLIWIISLVSLPQITTYGVNFDKILC 180
QY 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVITKLLHAGGQKRSKLTIFLVMAVF 240
DB 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVITKLLHAGGQKRSKLTIFLVMAVF 240
QY 241 LLTQMPFNLMKFIRSTHMEYYAMTSFHYTINWTEAIVLACLNPLVLYAFVSLKFRKNFW 300
DB 241 LLTQMPFNLMKFIRSTHMEYYAMTSFHYTINWTEAIVLACLNPLVLYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFSSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFSSASHNVEATSMFOL 342
RESULT 2
AAW54041
ID AAW54041 standard; Protein: 342 AA.
AC AAW54041;
XX
DT 07-AUG-1998 (first entry)
XX
XX Human HBMBU14 protein.
XX
KW Human; 7-transmembrane receptor; HBMBU14; infection; HIV; cancer; asthma;
KW anorexia; Parkinson's disease; acute heart failure; atherosclerosis;
KW osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
KW benign prostatic hypertrophy; neurological disorder; therapy;
KW Huntington's disease; Gilles de la Tourette's syndrome.
XX
OS Homo sapiens.
XX
XX EP834563-A2.
XX
XX PD 08-APR-1998.
XX
XX PE 23-SEP-1997; 97EP-0307428.
XX
XX PR 26-SEP-1996; 96US-0026669.
XX
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX PI Bergsma DJ, Ellis CE, Elshourbagy NA;
XX
XX WPI; 1998-208924/19.

DR N-PSDB; AAV24017.
XX
XX New isolated human 7-trans-membrane receptor, HBMBU14 - useful for
PT developing products for treating, e.g. infections, pain, cancers,
PT anorexia, hypotension, osteoporosis and asthma
XX
XX Claim 12; Fig 1; 36pp; English.
XX
XX This sequence is the human HBMBU14 protein of the invention. HBMBU14
CC is a human 7-transmembrane (TM) receptor. The products can be used for
CC treating or preventing conditions related to abnormal HBMBU14 expression
CC or activity, e.g. infections such as bacterial, fungal, protozoan and
CC viral infections especially infections caused by HIV-1 and HIV-2, pain,
CC cancers, anorexia, bulimia, asthma, Parkinson's disease, acute heart
CC failure, atherosclerosis, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma,
CC allergies, benign prostatic hypertrophy and psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression, delirium,
CC dementia or severe mental retardation, and dyskinesias, such as
CC Huntington's disease or Gilles de la Tourette's syndrome. The products
CC can also be used for diagnosing a disease or susceptibility to a disease
CC related to the expression of HBMBU14 and for identifying compounds which
CC bind to and activate or inhibit a receptor for the polypeptide.

SO Sequence 342 AA:
Query Match 100.0%; Score 1794; DB 19; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.4e-180; Indels 0; Gaps 0;
Matches 342; Conservative 0; Mismatches 0;
QY 1 MAEHDYHEDYGFSSFNDSOEHDQFQSKVFLPCMTLVFVCGVGNLSLVYISIFYH 60
DB 1 MAEHDYHEDYGFSSFNDSOEHDQFQSKVFLPCMTLVFVCGVGNLSLVYISIFYH 60
QY 61 KLSQLTDFVFLNPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
DB 61 KLSQLTDFVFLNPLADLVFVCTLPFMAVAGIHEWFGQVCKSLGITYTINFTSMIL 120
QY 121 TCITVDREFIVVKKATKANOAKRMWGKVTSLIWIISLVSLPQITTYGVNFDKILC 180
DB 121 TCITVDREFIVVKKATKANOAKRMWGKVTSLIWIISLVSLPQITTYGVNFDKILC 180
QY 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVITKLLHAGGQKRSKLTIFLVMAVF 240
DB 181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVITKLLHAGGQKRSKLTIFLVMAVF 240
QY 241 LLTQMPFNLMKFIRSTHMEYYAMTSFHYTINWTEAIVLACLNPLVLYAFVSLKFRKNFW 300
DB 241 LLTQMPFNLMKFIRSTHMEYYAMTSFHYTINWTEAIVLACLNPLVLYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFSSASHNVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSQWKSSEDNSKTFSSASHNVEATSMFOL 342
RESULT 3
AAV39366
ID AAV39366 standard; Protein: 342 AA.
AC AAV39366;
XX
XX DT 05-JAN-2000 (first entry)
XX
XX DE Platelet factor-4 (PF-4) receptor amino acid sequence.
XX
XX PF-4; platelet factor-4; alpha granules; collagen; thrombotic stimuli;
KW thrombosis; inflammatory activity; chemokine; PF-4 receptor; HBMBU14;
KW BONZO; TTMSTR; agonist; antagonist; HIV; AIDS; rheumatoid arthritis;
KW asthma; psoriasis; atherosclerosis; inflammatory disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO9950670-A1.

XX 07-OCT-1999.
 XX
 PD
 XX
 PF 26-MAR-1999; 99WO-GB00950.
 XX
 XX
 FR 27-MAR-1998; 98GB-0006677.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Macphree CH, Moores K, Berkhout TA;
 PI
 XX WPI; 1999-591378/50.
 DR
 DR N-PSDB; AAZ28362.
 XX
 XX Novel PF-4 receptor assays used to identify antagonists and agonists of
 PT the receptor for use in therapy -
 XX
 XX Example 1; Page 27-28; 35pp; English.
 XX

This sequence is the platelet factor-4 (PF-4) receptor amino acid sequence. PF-4 is a 70 residue polypeptide released from alpha-granules when platelets are activated by contacting collagen or other thrombotic stimuli. PF-4 promotes thrombosis at sites of platelet activation, and also exhibits several inflammatory activities. The carboxy terminal tripeptide of PF-4 is a potent chemotactic agent for monocytes. PF-4 is a CXc chemokine. The PF-4 receptor, also known as HMBMD4, TYWSTR and BONO2, is used in the methods of the invention. The invention relates to a novel screening method for identifying antagonists and agonists of the PF-4 receptor, involving using PF-4 and the PF-4 receptor together. PF-4 and the PF-4 receptor are used to identify further chemokine ligands for the receptor using a competitive binding assay and labeled PF-4. PF-4 used to identify neutralizing or activating antibodies to the PF-4 receptor for use in therapy. PF-4 can be used in a screening method for identifying an antagonist of the receptor. Antagonists and agonists may be used for therapeutic purposes, such as treatment of HIV, AIDS, rheumatoid arthritis, asthma, psoriasis, atherosclerosis, and other inflammatory diseases.

SQ Sequence 342 AA;

Query Match	100.0%	Score 1794	DB 20	Length 342
Best Local Similarity	100.0%	Pred. NO. 1.4e-180		
Matches 342	0	Mismatches 0	Indels 0	Gaps 0

QY	MAHXYDHEGYGSSFNDSQSEHOPLOFSKVFPCMLVYVYVGLGNSLTVYISLEFH	60
QY	1 MAHXYDHEGYGSSFNDSQSEHOPLOFSKVFPCMLVYVYVGLGNSLTVYISLEFH	60
QY	KIÖSLTDVFLVNLPLADLVFCVCTLPFMAVAGIHEWFGOVCKSLGIYTNFTSMIL	120
Db	61 KIÖSLTDVFLVNLPLADLVFCVCTLPFMAVAGIHEWFGOVCKSLGIYTNFTSMIL	120
QY	121 TCITTVRFIVVYKATATAYNOAKRMTGCKVTSLLIWTLSLVSPLPÖIITYGVPFLDLIC	180
Db	121 TCITTVRFIVVYKATATAYNOAKRMTGCKVTSLLIWTLSLVSPLPÖIITYGVPFLDLIC	180
QY	181 GYHDEAISTVYVATÖMTLGFPLPLIMTVCSVIIKTLLHAGFGÖKHRSKIIFFLVMAVF	240
Db	181 GYHDEAISTVYVATÖMTLGFPLPLIMTVCSVIIKTLLHAGFGÖKHRSKIIFFLVMAVF	240
QY	241 LTLÖMFENFLMKFRSTTHMEYVAMTSFPHITIMVTEAIALTRACLPVLYAFVSLKFRKNFM	300
Db	241 LTLÖMFENFLMKFRSTTHMEYVAMTSFPHITIMVTEAIALTRACLPVLYAFVSLKFRKNFM	300
QY	301 KLVKDIGCLPYLGVSÖHÖKMSBDSNKTTSASINVEATISMÖL 342	
Db	301 KLVKDIGCLPYLGVSÖHÖKMSBDSNKTTSASINVEATISMÖL 342	

RESULT 4	
AAW97783	
ID AAW97783	standard; Protein; 342 AA.
XX	

AC	AAM97783;
XX	
DT	21-MAY-1999 (first entry)
XX	
DE	Human HIV/SIV receptor protein Bonzo.
XX	
KW	SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
KX	human; G protein coupled receptor; chemokine receptor; AIDS;
KM	infection; virus transmission.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 53
FT	/note= "encoded by TG"
FT	Misc-difference 9..71
FT	/note= "encoded by TG"
FT	Misc-difference 102
FT	/note= "encoded by CG"
XX	
PN	WO9903868-A1.
XX	
PD	28-JAN-1999.
XX	
PF	17-JUL-1998; 98WO-US14857.
XX	
PR	17-JUL-1997; 97US-0896155.
XX	
PA	(UYNV) UNIV NEW YORK STATE.
PI	Deng H, Kewalramani VN, Littman DR, Unutmaz D;
XX	
DR	WPI: 1999-132164/11.
N-PSTB:	AAK07289.
XX	
PT	New nucleic acid encoding the human translocation promoter Bonzo -
PT	used to screen for potential agents for treating acquired immune
XX	deficiency syndrome
PS	Claim 4; Page 78-79; 97pp; English.
XX	
CC	This is the amino acid sequence of human Bonzo, a novel HIV/SIV
CC	translocation promoting agent that acts in conjunction with CD4 to
CC	serve as a receptor for the entry into a cell of a virus having a
CC	specific viral envelope glycoprotein. Bonzo is a member of the
CC	7-transmembrane G-protein coupled receptor family, is closely
CC	related to the chemokine receptor family, and is expressed in
CC	lymphoid tissues. The invention provides the amino acid sequences
CC	(see AAM97783-88) and DNA sequences (see AAK07289-94) of human,
CC	African green monkey and pig-tailed macaque Bonzo and Bob (brother
CC	of Bonzo) translocation promoting agents. These novel receptors
CC	were identified using an expression cloning strategy. They were
CC	found to be used by particular strains of HIV-2 and M-tropic HIV-1.
CC	The invention also includes: mammalian cells transfected with Bonzo
CC	and/or Bob and human CD4, which can be used to screen potential
CC	therapeutic agents and identify ligands; antibodies to Bonzo, which
CC	can be used therapeutically, e.g. as antagonists or to target
CC	toxins or radioisotopes to HIV-permissive cells; transgenic
CC	animals; and antisense and ribozyme molecules, which may also be
CC	used therapeutically, particularly expressed from a gene therapy
CC	vector.
XX	
SQ	Sequence 342 AA;
XX	
Query Match	100.0%; Score 1794; DB 20; Length 342;
Best Local Similarity	100.0%; Pident No. 1,4e-180;
Matches 342: Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHDHEDYGFSSFNDSQSEEHQDFLQPSKFLPCMFLVYFVCGVGNLSLVLYISLTFYH 60

Db 1 MAEHDHEDYGFSSFNDSQSEEHQDFLQPSKFLPCMFLVYFVCGVGNLSLVLYISLTFYH 60

QY 61 KLSQSLDVLVFNLPPLADLVFVCTLPFPMAYAGIHEMVPQVQWCKSLSLGIYTNFTSMIL 120

```

Db      |||||
61      KLSSTDFEVLNPLADLVFVCTLPFMAYAGIHEWVFGVCKSLGITYTINFTSMIL 120
QY      121 TCIYVDRITVVVKATKAVNQAKRTWGTSLIWIISLVSLPQIITYGVNFNDKILIC 180
Db      121 TCIYVDRITVVVKATKAVNQAKRTWGTSLIWIISLVSLPQIITYGVNFNDKILIC 180
QY      181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFOKHSKTIIFLVMAVF 240
Db      181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFOKHSKTIIFLVMAVF 240
QY      241 LITQMPFNLKMFIRSTHWEYAMTSFHYTIMVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
Db      241 LITQMPFNLKMFIRSTHWEYAMTSFHYTIMVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
QY      301 KLVNDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342
Db      301 KLVNDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342

```

RESULT 5

AC80125
AAG80125 standard; Protein: 342 AA.

AC AAG80125;

DT 17-JAN-2002 (first entry)

DE Human CXCR6 protein.

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 antineumatic; antitubercic.

XX Homo sapiens.

OS WO200172830-A2.

PN 04-OCT-2001.

PD 02-APR-2001; 2001WO-EP03708.

PE 31-MAR-2000; 2000DE-1016013.

PR (IPFP-) IPF PHARM GMBH.

PA (FORS/) FORSMANN U.

PI Forsmann W, Adermann K, Heitland A, Spodsberg N;

WPI: 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands,
 PT useful for detecting tumors, inflammation etc., also therapeutic use of
 PT ligand inhibitors

PS Disclosure; Page 13; 26pp; German.

CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antineumatic, antitubercic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and

CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention.

XX SQ Sequence 342 AA;

Query Match 100.0%; Score 1794; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1,4e-180;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 MAEHDYHDYGFSSFNDSOEHODLOFSKVFLPCMYLVFVCGLVGNSLVVISIFVH 60
Db      1 MAEHDYHDYGFSSFNDSOEHODLOFSKVFLPCMYLVFVCGLVGNSLVVISIFVH 60
QY      61 KLSSTDFEVLNPLADLVFVCTLPFMAYAGIHEWVFGVCKSLGITYTINFTSMIL 120
Db      61 KLSSTDFEVLNPLADLVFVCTLPFMAYAGIHEWVFGVCKSLGITYTINFTSMIL 120
QY      121 TCIYVDRITVVVKATKAVNQAKRTWGTSLIWIISLVSLPQIITYGVNFNDKILIC 180
Db      121 TCIYVDRITVVVKATKAVNQAKRTWGTSLIWIISLVSLPQIITYGVNFNDKILIC 180
QY      181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFOKHSKTIIFLVMAVF 240
Db      181 GYHDEAISTVVLATQMTLGFPLPLTMIVCYSVIIKTLHAGGFOKHSKTIIFLVMAVF 240
QY      241 LITQMPFNLKMFIRSTHWEYAMTSFHYTIMVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
Db      241 LITQMPFNLKMFIRSTHWEYAMTSFHYTIMVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
QY      301 KLVNDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342
Db      301 KLVNDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342

```

RESULT 6

AAG79091
AAG79091 standard; Protein: 342 AA.

AC AAG79091;

DT 10-DEC-2001 (first entry)

DE Amino acid sequence of a human polypeptide.

KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV;
 KW gp120; C-type lectin; ICAM3; HIV entry; T cell; macrophage;
 KW HIV infection.

XX Homo sapiens.

OS WO200164752-A2.

PN 07-SEP-2001.

PD 28-FEB-2001; 2001WO-US06322.

PE 02-MAR-2000; 2000US-0517605.

PR (UYNY) UNIV NEW YORK STATE.

PA (UYNI-) UNIV NIJMEGEN.

PI Litman DR, Kwon D, Van Kooyk Y, Geljtenbeek T;

WPI: 2001-602565/68.

XX An antibody for the treatment or prevention of HIV-infection comprises
 PT a gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding
 PT of DC-SIGN due to concomitant conformational change

PS Disclosure; Page 123-124; 131pp; English.

CC The specification describes an antibody which is specific for an
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN

CC or is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin.
 CC DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human polypeptide.
 CC which is used in the course of the invention.

XX Sequence 342 AA;

Query Match 100.0%; Score 1794; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.4e-180;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHDYEDYGFSSFNDSQSEHODFLQFSKVELPCMYLVFVCGLVGNSLVVISIETH 60
 1 MAEHDYEDYGFSSFNDSQSEHODFLQFSKVELPCMYLVFVCGLVGNSLVVISIETH 60
 QY KIOSLDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
 61 KIOSLDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
 Db 121 TCITVDFEIVVATKAYNOQAKRMWGKTSLLIWIISLVSLPQIYGNVFNLDKLC 180
 121 TCITVDFEIVVATKAYNOQAKRMWGKTSLLIWIISLVSLPQIYGNVFNLDKLC 180
 QY 181 GYHDEAISTVVALTOMTGFPLIMIVCYSVIITKLHAGGFQKRSKIIFLVMAVF 240
 181 GYHDEAISTVVALTOMTGFPLIMIVCYSVIITKLHAGGFQKRSKIIFLVMAVF 240
 Db 241 LITOMPENLMKFFIRSTHWEYAMTSFYITMVEATAYLRACNLPVYAVSLKFRKNF 300
 241 LITOMPENLMKFFIRSTHWEYAMTSFYITMVEATAYLRACNLPVYAVSLKFRKNF 300
 QY 301 KLVKDIGCLPYLGVSQWKSSEDSKTFSSAHNVEATSMFQL 342
 301 KLVKDIGCLPYLGVSQWKSSEDSKTFSSAHNVEATSMFQL 342
 Db 301 KLVKDIGCLPYLGVSQWKSSEDSKTFSSAHNVEATSMFQL 342

RESULT 7
 AAG67239
 ID AAG67239 standard; Protein: 342 AA.

XX AAG67239;

13-NOV-2001 (first entry)

XX Amino acid sequence of human chemokine receptor Bonzo.
 XX

KW Human: chemokine receptor: CCR11; G protein coupled receptor;
 KW inflammatory disease; Rheumatoid arthritis; inflammatory bowel disease;
 KW asthma; angiodysplasia; arteriosclerosis; vascular association disease;
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
 KW left ventricular diastolic dysfunction; migraine; preterm labour;
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
 KW myocardial infarction; congestive heart failure; endometriosis; Bonzo;
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.

OS Homo sapiens.

XX W0200166598-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US07073.

XX 03-MAR-2000; 2000US-0186928.

XX 03-MAR-2000; 2000US-0187231.

XX (ICOS-) ICOS CORP.

XX Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
 PI WPL: 2001-541918/60.
 DR N-PSDB: AAH77725.

XX An isolated polynucleotide encoding the chemokine receptor CCR11,
 PT useful for treating rheumatoid arthritis, inflammatory bowel disease,
 PT asthma, angiodysplasia, arteriosclerosis, cardiac arrhythmias, Raynaud's
 PT phenomenon and migraine -

XX Example 8; Page 109-110; 110pp; English.

XX The present sequence represents the human chemokine receptor Bonzo. The
 CC specification also describes the human chemokine receptor CCR11.
 CC CCR11 is a member of the G protein coupled receptor family. A CCR11
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
 CC expression or biological activity, is useful for treating many
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
 CC bowel disease, and asthma. They are also useful for treating
 CC angiodysplasia, arteriosclerosis, vascular association diseases which may
 CC include but are not limited to hypertension, angina pectoris, cardiac
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
 CC heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
 CC pulmonary vascular disease.

XX Sequence 342 AA;

Query Match 100.0%; Score 1794; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.4e-180;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHDYEDYGFSSFNDSQSEHODFLQFSKVELPCMYLVFVCGLVGNSLVVISIETH 60
 1 MAEHDYEDYGFSSFNDSQSEHODFLQFSKVELPCMYLVFVCGLVGNSLVVISIETH 60
 Db 61 KIOSLDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
 61 KIOSLDFVFLVNLPLADLVFVCTLPFWAYAGIHEWVGQVCKSLGITYINFTSMIL 120
 QY 121 TCITVDFEIVVATKAYNOQAKRMWGKTSLLIWIISLVSLPQIYGNVFNLDKLC 180
 121 TCITVDFEIVVATKAYNOQAKRMWGKTSLLIWIISLVSLPQIYGNVFNLDKLC 180
 Db 181 GYHDEAISTVVALTOMTGFPLIMIVCYSVIITKLHAGGFQKRSKIIFLVMAVF 240
 181 GYHDEAISTVVALTOMTGFPLIMIVCYSVIITKLHAGGFQKRSKIIFLVMAVF 240
 QY 241 LITOMPENLMKFFIRSTHWEYAMTSFYITMVEATAYLRACNLPVYAVSLKFRKNF 300
 241 LITOMPENLMKFFIRSTHWEYAMTSFYITMVEATAYLRACNLPVYAVSLKFRKNF 300
 Db 301 KLVKDIGCLPYLGVSQWKSSEDSKTFSSAHNVEATSMFQL 342
 301 KLVKDIGCLPYLGVSQWKSSEDSKTFSSAHNVEATSMFQL 342

RESULT 8
 AAU04032
 ID AAU04032 standard; Protein: 342 AA.

XX AAU04032;

XX 23-OCT-2001 (first entry)

XX Human HIV translocation agent, Bonzo.

XX Human: Bonzo; human immunodeficiency virus; HIV translocating agent;
 KW CD4; BOB; Brother of Bonzo; acquired immunodeficiency syndrome;
 KW AIDS.

XX


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OS Homo sapiens.
XX Key Location/Qualifiers
FH Domain 1..33
FT Domain /label= Extracellular_domain
FT Misc-difference 53
FT /note= "Encoded by TG"
FT Misc-difference 71
FT /note= "Encoded by TG"
FT Domain /note= "Encoded by TG"
FT /label= Extracellular_domain
FT Misc-difference 106
FT /note= "Encoded by CG"
FT Domain /label= Extracellular_domain
FT Domain /label= Extracellular_domain
FT Domain 250..270
FT Domain /label= Extracellular_domain
XX US6251582-B1.
XX PD 26-JUN-2001.
XX 16-JUL-1998; 98US-0116498.
XX 17-JUL-1997; 97US-0052827.
XX (UYNX ) UNIV NEW YORK STATE.
XX PA
XX PI Littman DR, Deng H, Unutmaz D, Kewalramani VN:
XX WPI: 2001-424455/45.
XX DR N-PSDB: AAS04032.
XX PT Identifying an agent for treating AIDS comprises administering a
XX PT potential therapeutic agent to a cell expressing human CD4 and primate
XX PT Bonzo or BOB and contacting the cell with a virus pseudotyped with an
XX PT HIV envelope glycoprotein.
XX Example 1; Fig 2C; 41pp; English.
XX PS
XX CC The sequence represents a novel HIV (human immunodeficiency virus)
XX CC translocating agent, Bonzo. The invention relates to selecting an agent
XX CC that may be used in treating acquired immunodeficiency syndrome (AIDS)
XX CC comprises administering a potential therapeutic agent to a cell
XX CC expressing human CD4 and primate Bonzo or BOB (Brother Of Bonzo),
XX CC contacting the cell with a virus pseudotyped with an HIV envelope
XX CC glycoprotein, and measuring the cell's ability to resist infection. The
XX CC method is useful for selecting or identifying an agent, which can be used
XX CC in treating AIDS.
XX Sequence 342 AA:
Query Match 100.0%; Score 1794; DB 22; Length 342;
Best local Similarity 100.0%; Pred. No. 1.4e-180;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEHDYHEDYGFSSFNDSQEEHQDLQFSKVFLLPCMYLVVFCGLVGNLSLVISIFYH 60
DB 1 MAEHDYHEDYGFSSFNDSQEEHQDLQFSKVFLLPCMYLVVFCGLVGNLSLVISIFYH 60
QY 61 KIOSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGVGMCKSLGITYINFTSMILL 120
DB 61 KIOSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGVGMCKSLGITYINFTSMILL 120
QY 121 TCITVDFEIVVAKATRAYNOQAKRMWGKVTSLLIWISLSVLPDIYGNVFNLDKLC 180
DB 121 TCITVDFEIVVAKATRAYNOQAKRMWGKVTSLLIWISLSVLPDIYGNVFNLDKLC 180
QY 181 GYHDEAISTVVLATQMTLGFPLLTMIWICYSVIITKLLHAGGFQKHSIKIIFLVMAVF 240
DB 181 GYHDEAISTVVLATQMTLGFPLLTMIWICYSVIITKLLHAGGFQKHSIKIIFLVMAVF 240
QY 241 LITQMFNPLMKFIRSTHMEYVAMTSFHYTITMVEALAYLACINPVLIVAVSLKFRNF 300
DB 241 LITQMFNPLMKFIRSTHMEYVAMTSFHYTITMVEALAYLACINPVLIVAVSLKFRNF 300
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DB 241 LITQMFNPLMKFIRSTHMEYVAMTSFHYTITMVEALAYLACINPVLIVAVSLKFRNF 300
QY 301 KLVKDIGCLPYLGVSHOWKSSSEDSNKFSSASHVVEATSMFOL 342
DB 301 KLVKDIGCLPYLGVSHOWKSSSEDSNKFSSASHVVEATSMFOL 342
RESULT 9
ID AAB68422 standard; Protein: 342 AA.
XX AAB68422
XX AC AAB68422;
XX DT 23-JUL-2001 (first entry)
XX DE Amino acid sequence of a human Bonzo polypeptide.
XX KW Bonzo; CXK chemokine receptor; inflammatory disease; cancer; infection;
XX KW Sexckine; spleen extracted chemokine.
XX OS Homo sapiens.
XX PN W0200137872-A1.
XX PD 31-MAY-2001.
XX PF 22-NOV-2000; 2000MO-US32206.
XX PR 24-NOV-1999; 99US-0449437.
XX (MILL-) MILLENNIUM PHARM INC.
XX PI Briskin MJ, Murphy KE, Wilbanks AM, Wu L;
XX DR WPI: 2001-343947/36.
XX DR N-PSDB: AAF85364.
XX PT Identifying agents (especially antibodies) which bind to the CXK
XX PT chemokine receptor Bonzo, and which may be used to treat e.g. cancers
XX PT and inflammation.
XX PS Example 1; Fig 2; 191pp; English.
XX CC The present sequence represents a human Bonzo polypeptide. Bonzo is a
XX CC CXK chemokine receptor. The specification describes a method for
XX CC identifying agents (especially antibodies) which bind to Bonzo and
XX CC inhibit the binding of a ligand (especially SEXckine (spleen extracted
XX CC chemokine)) and the agents per se. The agents identified may be used
XX CC for the treatment of a disorder/disease related to aberrant Bonzo
XX CC expression and activity, such as inflammatory disease, cancers and/or
XX CC infections (e.g. viral, bacterial and fungal infections).
XX Sequence 342 AA:
Query Match 100.0%; Score 1794; DB 22; Length 342;
Best local Similarity 100.0%; Pred. No. 1.4e-180;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEHDYHEDYGFSSFNDSQEEHQDLQFSKVFLLPCMYLVVFCGLVGNLSLVISIFYH 60
DB 1 MAEHDYHEDYGFSSFNDSQEEHQDLQFSKVFLLPCMYLVVFCGLVGNLSLVISIFYH 60
QY 61 KIOSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGVGMCKSLGITYINFTSMILL 120
DB 61 KIOSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWFGVGMCKSLGITYINFTSMILL 120
QY 121 TCITVDFEIVVAKATRAYNOQAKRMWGKVTSLLIWISLSVLPDIYGNVFNLDKLC 180
DB 121 TCITVDFEIVVAKATRAYNOQAKRMWGKVTSLLIWISLSVLPDIYGNVFNLDKLC 180
QY 181 GYHDEAISTVVLATQMTLGFPLLTMIWICYSVIITKLLHAGGFQKHSIKIIFLVMAVF 240
DB 181 GYHDEAISTVVLATQMTLGFPLLTMIWICYSVIITKLLHAGGFQKHSIKIIFLVMAVF 240
```

Db 181 GHDEAISTVVLATQMTLGFPLPLTMIVCSYIITKLLAHAGGQKHSILKIIFLVAVF 240
 QY 241 LLTQMPFNLMKFIKSTHMEYAMTSFHTIIVTEALVLRACLPVLYAFVSLKFRKNFW 300
 Db 241 LLTQMPFNLMKFIKSTHMEYAMTSFHTIIVTEALVLRACLPVLYAFVSLKFRKNFW 300
 QY 301 KLVKDICGLPYLGVS HQKSSSEDSKTFSSASHNEATSMFOL 342
 Db 301 KLVKDICGLPYLGVS HQKSSSEDSKTFSSASHNEATSMFOL 342

RESULT 10
 AAW97785
 ID AAW97785 standard; Protein: 342 AA.
 AC AAW97785;
 XX 21-MAY-1999 (first entry)
 DT Pig-tailed macaque HIV/SIV receptor protein Bonzo.
 KW SIV receptor; HIV receptor; Bonzo: translocation promoting agent;
 KM G protein coupled receptor; chemokine receptor; AIDS; Infection;
 XX virus transmission; pig-tailed macaque.
 OS Macaca nemestrina.
 XX
 XX WO9903888-A1.
 PN 28-JAN-1999.
 PD 17-JUL-1998; 98WO-US14857.
 XX 17-JUL-1997; 97US-0896155.
 PR 17-JUL-1997; 97US-0896155.
 XX (UYNV) UNIV NEW YORK STATE.
 PA Deng H, Kewalramani VN, Littman DR, Unutmaz D;
 PI WPI: 1999-132164/11.
 DR N-PSDB: AAX07291.
 XX
 PT New nucleic acid encoding the human translocation promoter Bonzo -
 PT used to screen for potential agents for treating acquired immune
 PT deficiency syndrome
 XX
 XX Disclosure: Page 82-83; 97pp; English.

This is the amino acid sequence of pig-tailed macaque Bonzo, a novel HIV/SIV translocation promoting agent that acts in conjunction with CD4 to serve as a receptor for the entry into a cell of a virus having a specific viral envelope glycoprotein. Bonzo is a member of the 7-transmembrane G-protein coupled receptor family, is closely related to the chemokine receptor family, and is expressed in lymphoid tissues. The invention provides the amino acid sequences (see AAW97783-88) and DNA sequences (see AAX07289-94) of human, African green monkey and pig-tailed macaque Bonzo and Bob (brother of Bonzo) translocation promoting agents. These novel receptors were identified using an expression cloning strategy. They were found to be used by particular strains of HIV-2 and M-tropic HIV-1. The invention also includes: mammalian cells transfected with Bonzo and/or Bob and human CD4, which can be used to screen potential therapeutic agents and identify ligands; antibodies to Bonzo, which can be used therapeutically, e.g. as antagonists or to target toxins or radioisotopes to HIV-permissive cells; transgenic animals; and antisense and ribozyme molecules, which may also be used therapeutically, particularly expressed from a gene therapy vector.

Sequence 342 AA:
 Query Match 96.4%; Score 1730; DB 20; Length 342;
 Best Local Similarity 95.6%; Pred. No. 8e-174;

Matches 327; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MAEHYEDYGFSSFNDSOEHDPLQFSKVPFCMAYIVYVCGVGNLSLVISTFYH 60
 Db 1 MAEHYEDYGLNFSNDSOEHDPLQFSKVPFCMAYIVYVCGVGNLSLVISTFYH 60
 QY 61 KLSLTDFVLNPLADLVVCTLPFAVYAGIHMEVGVCKSLGIYTFNFTSMIL 120
 Db 61 KLSLTDFVLNPLADLVVCTLPFAVYAGIHMEVGVCKSLGIYTFNFTSMIL 120
 QY 121 TCITVDRFIVVKATKAYNOAKRMWGVKTSLLIWIISLVSLPQIIVGVNEMDLKIC 180
 Db 121 TCITVDRFIVVKATKAYNOAKRMWGVKTSLLIWIISLVSLPQIIVGVNEMDLKIC 180
 QY 181 GHDEAISTVVLATQMTLGFPLPLTMIVCSYIITKLLAHAGGQKHSILKIIFLVAVF 240
 Db 181 GHDEAISTVVLATQMTLGFPLPLTMIVCSYIITKLLAHAGGQKHSILKIIFLVAVF 240
 QY 241 LLTQMPFNLMKFIKSTHMEYAMTSFHTIIVTEALVLRACLPVLYAFVSLKFRKNFW 300
 Db 241 LLTQMPFNLMKFIKSTHMEYAMTSFHTIIVTEALVLRACLPVLYAFVSLKFRKNFW 300
 QY 301 KLVKDICGLPYLGVS HQKSSSEDSKTFSSASHNEATSMFOL 342
 Db 301 KLVKDICGLPYLGVS HQKSSSEDSKTFSSASHNEATSMFOL 342

RESULT 11
 AAU04034
 ID AAU04034 standard; Protein: 342 AA.
 AC AAU04034;
 XX 23-OCT-2001 (first entry)
 DT Pig-tailed macaque SIV translocation agent, Bonzo.
 XX
 DE Pig-tailed macaque; Bonzo: simian immunodeficiency virus;
 KM SIV translocation agent; CD4; BOB: Brother of Bonzo;
 KW acquired immunodeficiency syndrome; AIDS; SIV; HIV.
 XX
 OS Macaca nemestrina.
 XX
 XX US6251582-B1.
 PN 26-JUN-2001.
 PD 16-JUL-1998; 98US-0116458.
 XX 16-JUL-1997; 97US-0052827.
 PR 17-JUL-1997; 97US-0052827.
 XX (UYNV) UNIV NEW YORK STATE.
 PA Littman DR, Deng H, Unutmaz D, Kewalramani VN;
 PI WPI: 2001-424455/45.
 DR N-PSDB: AAS07616.
 XX
 PT Identifying an agent for treating AIDS comprises administering a
 PT potential therapeutic agent to a cell expressing human CD4 and primate
 PT Bonzo or BOB and contacting the cell with a virus pseudotyped with an
 PT HIV envelope glycoprotein -
 XX
 PS Example 1: Column 43-46; 41pp; English.
 XX
 XX The sequence represents a novel SIV (Simian immunodeficiency virus)
 XX translocating agent, Bonzo. The invention relates to selecting an agent
 XX that may be used in treating acquired immunodeficiency syndrome (AIDS)
 CC comprising administering a potential therapeutic agent to a cell
 CC expressing human CD4 and primate Bonzo or BOB (Brother of Bonzo),
 CC contacting the cell with a virus pseudotyped with an HIV envelope
 CC glycoprotein, and measuring the cell's ability to resist infection. The
 CC method is useful for selecting or identifying an agent, which can be used

Query Match	96.4%	Score 1730;	DB 22;	Length 342;
Best Local Similarity	95.6%	Pred. No. 8e-174;		
Matches 327;	Conservative 7;	Mismatches 8;	Indels 0;	Gaps 0;
1 MAEHDEHEDGFSSEFNDSOEHOEDFOESKVFLLPCWLVYVCGIGVNSLVVISTFPH 60	1 MAEHDEHEDGFSSEFNDSOEHOEDFOESKVFLLPCWLVYVCGIGVNSLVVISTFPH 60			
1 MAEHDEHEDGFSSEFNDSOEHOEDFOESKVFLLPCWLVYVCGIGVNSLVVISTFPH 60	1 MAEHDEHEDGFSSEFNDSOEHOEDFOESKVFLLPCWLVYVCGIGVNSLVVISTFPH 60			
61 KLSLSTVFLVNLPLADLVFVCTLPFAVAGIHEWVFGVWCKSLGITYINFTSMIL 120	61 KLSLSTVFLVNLPLADLVFVCTLPFAVAGIHEWVFGVWCKSLGITYINFTSMIL 120			
121 TCTIVDFEPIVVKTKAVNOAKRMWGKVTSLLIWVISTLVSPQIIYGVNFMNDKIC 180	121 TCTIVDFEPIVVKTKAVNOAKRMWGKVTSLLIWVISTLVSPQIIYGVNFMNDKIC 180			
121 TCTIVDFEPIVVKTKAVNOAKRMWGKVTSLLIWVISTLVSPQIIYGVNFMNDKIC 180	121 TCTIVDFEPIVVKTKAVNOAKRMWGKVTSLLIWVISTLVSPQIIYGVNFMNDKIC 180			
181 GYHDEAISTVVLATQMTLGFELPLFTMIVCYSVIIKTLHAGFGOKHRSKLIIFLVMAVF 240	181 GYHDEAISTVVLATQMTLGFELPLFTMIVCYSVIIKTLHAGFGOKHRSKLIIFLVMAVF 240			
181 GYHDEAISTVVLATQMTLGFELPLFTMIVCYSVIIKTLHAGFGOKHRSKLIIFLVMAVF 240	181 GYHDEAISTVVLATQMTLGFELPLFTMIVCYSVIIKTLHAGFGOKHRSKLIIFLVMAVF 240			
241 LITQMPNINAKFISTHMEYVAMTSFHTIMVTAIAYLRCLNPVLYAFVSLKFRKNFW 300	241 LITQMPNINAKFISTHMEYVAMTSFHTIMVTAIAYLRCLNPVLYAFVSLKFRKNFW 300			
241 LITQMPNINAKFISTHMEYVAMTSFHTIMVTAIAYLRCLNPVLYAFVSLKFRKNFW 300	241 LITQMPNINAKFISTHMEYVAMTSFHTIMVTAIAYLRCLNPVLYAFVSLKFRKNFW 300			
301 KLVKDICLPYLGVSHOWKSESDNSKTFESASHNVEATSMFOL 342	301 KLVKDICLPYLGVSHOWKSESDNSKTFESASHNVEATSMFOL 342			
301 KLVKDICLPYLGVSHOWKSESDNSKTFESASHNVEATSMFOL 342	301 KLVKDICLPYLGVSHOWKSESDNSKTFESASHNVEATSMFOL 342			
AAW97784 standard; Protein: 342 AA.	AAW97784 standard; Protein: 342 AA.			
AAW97784	AAW97784			
AAW97784	AAW97784			
21-MAY-1999 (first entry)	21-MAY-1999 (first entry)			
African green monkey HIV/SIV receptor protein Bonzo.	African green monkey HIV/SIV receptor protein Bonzo.			
SIV receptor; HIV receptor; Bonzo: translocation promoting agent;	SIV receptor; HIV receptor; Bonzo: translocation promoting agent;			
G protein coupled receptor; chemokine receptor; AIDS; infection;	G protein coupled receptor; chemokine receptor; AIDS; infection;			
virus transmission; African green monkey.	virus transmission; African green monkey.			
Cercopithecus aethiops.	Cercopithecus aethiops.			
WC0903888-A1.	WC0903888-A1.			
28-JAN-1999.	28-JAN-1999.			
17-JUL-1998; 98WO-US14857.	17-JUL-1998; 98WO-US14857.			
17-JUL-1997; 97US-0896155.	17-JUL-1997; 97US-0896155.			
(UNYV) UNIV NEW YORK STATE.	(UNYV) UNIV NEW YORK STATE.			
Deng H, Kewalramani VN, Littman DR, Unutmaz D;	Deng H, Kewalramani VN, Littman DR, Unutmaz D;			
WPI; 1999-132164/11.	WPI; 1999-132164/11.			
N-PSDB; AAX07290.	N-PSDB; AAX07290.			
New nucleic acid encoding the human translocation promoter Bonzo -	New nucleic acid encoding the human translocation promoter Bonzo -			
used to screen for potential agents for treating acquired immune	used to screen for potential agents for treating acquired immune			
deficiency syndrome	deficiency syndrome			
Disclosure; Page 80-81; 97pp; English.	Disclosure; Page 80-81; 97pp; English.			
This is the amino acid sequence of African green monkey Bonzo, a	This is the amino acid sequence of African green monkey Bonzo, a			
novel HIV/SIV translocation promoting agent that acts in conjunction	novel HIV/SIV translocation promoting agent that acts in conjunction			
with CD4 to serve as a receptor for the entry into a cell of a virus	with CD4 to serve as a receptor for the entry into a cell of a virus			

	CC	having specific viral envelope glycoprotein. Bonzo is a member of
	CC	the 7-transmembrane G-protein coupled receptor family, is closely
	CC	related to the chemokine receptor family, and is expressed in
	CC	lymphoid tissues. The invention provides the amino acid sequences
	CC	(see AA097783-88) and DNA sequences (see AX07289-94) of human,
	CC	African green monkey and pig-tailed macaque Bonzo and Bob (brother
	CC	of Bonzo) translocation promoting agents. These novel receptors
	CC	were identified using an expression cloning strategy. They were
	CC	found to be used by particular strains of HIV-2 and M-tropic HIV-1.
	CC	The invention also includes: mammalian cells transfected with Bonzo
	CC	and/or Bob and human CD4, which can be used to screen potential
	CC	therapeutic agents and identify ligands; antibodies to Bonzo, which
	CC	can be used therapeutically, e.g. as antagonists or to target
	CC	toxins or radiotopes to HIV-permissive cells; transgenic
	CC	animals; and antisense and ribozyme molecules, which may also be
	CC	used therapeutically, particularly expressed from a gene therapy
	CC	vector.
XX	Sequence	342 AA;
SQ	Query Match	95.7%; Score 1717; DB 20; Length 342;
	Best Local Similarity	95.3%; Pred. No. 1.9e-172;
	Matches	326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
OY	1	MAEHDIHEDYGFSSFNDSOEHOEHLQFSKVPFLPCMYLVFCGLVGNLSLVLISIFPH 60
Dd	1	MAEDHDHEDGDFNSFNSOEHODLFQFSKVFLPCMYLVFVGILVGNLSLVLISIFPH 60
OY	61	KLOSITGVFLVNLPLADLVFVCTLPENAVAGIHFWVGOWVCKSLIGITYNFTSMIL 120
Dd	61	KLOSITGVFLVNLPLADLVFVCTLPENAVACIHEWIRIGOWCKTLGLIYTINFTSMIL 120
OY	121	TCLTVDFRIFYVKATKAYNOQAKRMKGKVTSLLIWVISLLVSLEPQIIYGWFMIDKLIC 180
Dd	121	TCLTVDFRIYVVKAFKAYNOQAKRMKGKVICLLIWVISLLVSLEPQIIYGWFMIDKLIC 180
OY	181	GYNHEALSTVLAOMTIGFELPLTMIVCVSVLIKTLHAHGGRKRSKIIFLVNAVF 240
Dd	181	GYNHEELSTVLAOMTIGFELPLAMIVCVSVLIKTLHAHGGRKRSKIIFLVNAVF 240
OY	241	LLTOMPRLNLMKFIRSTHMEYYAMTSFYHTIMVTEAIAIYLACLAPVLYAEVSLFKRNFM 300
Dd	241	LTTGPENLVKLIIRSTHMEYYAMTSFYHTIIVEFAIALYLRACLNRPVLYAFASLKFRKNFM 300
OY	301	KLYKDTCGLPYLGYSHQWKSSSDNSKTFPSASHNVETASMFL 342
Dd	301	KLYKDTCGLPYLGYSHQWKSSSDNSKTFPSASHNVETASMFL 342
<hr/>		
RESULT 13		
ID	AAU04033	standard; Protein: 342 AA.
XX	AAU04033:	
AC	23-OCT-2001	(first entry)
XX		
DT		
XX		
DE		Green monkey SIV translocation agent, Bonzo.
XX		
KM		Monkey; Bonzo; simian immunodeficiency virus; SIV translocating agent;
KW		CD4; BOB; Brother of Bonzo; acquired immunodeficiency syndrome;
KM		AIDS; SIV; HIV.
OS		Cercopithecus aethiops.
PN	US6251582-B1.	
PD	26-JUN-2001.	
PF	16-JUL-1998;	98US-0116498.
DR	17-JUL-1997;	97US-0052827.

PA (UUNY) UNIV NEW YORK STATE.
 XX
 PI Littman DR, Deng H, Unutmaz D, Kewalramani VN;
 XX
 DR WPI: 2001-424455/45.
 DR N-PSDB: AAS07615.
 XX
 PT Identifying an agent for treating AIDS comprises administering a
 PT potential therapeutic agent to a cell expressing human CD4 and primate
 PT Bonzo or BOB and contacting the cell with a virus pseudotyped with an
 PT HIV envelope glycoprotein.
 XX
 PS Example 1; Column 41-42; 41pp; English.
 XX
 CC The sequence represents a novel HIV (Simian immunodeficiency virus)
 CC translocating agent, Bonzo. The invention relates to selecting an agent
 CC that may be used in treating acquired immunodeficiency syndrome (AIDS)
 CC comprising administering a potential therapeutic agent to a cell
 CC expressing human CD4 and primate Bonzo or BOB (Brother Of Bonzo),
 CC contacting the cell with a virus pseudotyped with an HIV envelope
 CC glycoprotein, and measuring the cell's ability to resist infection. The
 CC method is useful for selecting or identifying an agent, which can be used
 CC in treating AIDS.
 CC
 SQ Sequence 342 AA;
 XX
 Query Match 95.7%; Score 1717; DB 22; Length 342;
 Best Local Similarity 95.3%; Pred. No. 1.9e-172;
 Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 OY 1 MAEHYHEDYGFSSFNDSOEHOEFLQFSKYVFLPCMYLVFVCGLVGNSLVVISIFYH 60
 DB 1 MAEYHYEDNGFNPNSSDSEHODEFLQFSKYVFLPCMYLVFVCGLVGNSLVVISIFYH 60
 OY 61 KLOSLTDFVLNPLADLVFVCTLPFAVAGIHEWFGQVCKSLGITYINFTSMIL 120
 DB 61 KLOSLTDFVLNPLADLVFVCTLPFAVAGIHEWFGQVCKSLGITYINFTSMIL 120
 OY 121 TCITVDFRIYVVKATKAYNOQAKRMWGKVTSLIIVVSLVSLPQIITYGWVFNLDKILC 180
 DB 121 TCITVDFRIYVVKATKAYNOQAKRMWGKVTSLIIVVSLVSLPQIITYGWVFNLDKILC 180
 OY 181 GYHDEAISTVVLATQMTLGFELPLITMIVCYSVIIKTLHAGGFOKHSKLIIFLVMAVF 240
 DB 181 GYHDEAISTVVLATQMTLGFELPLITMIVCYSVIIKTLHAGGFOKHSKLIIFLVMAVF 240
 OY 241 LLTQMPENLMKFIKSTHMEYYAMTSFHTITMTEALATLRACLNVPVLYAFVSLKFRKNF 300
 DB 241 LLTQMPENLMKFIKSTHMEYYAMTSFHTITMTEALATLRACLNVPVLYAFVSLKFRKNF 300
 OY 301 KLVKDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342
 DB 301 KLVKDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342
 RESULT 14
 ID AAY23825
 XX AAY23825 standard; Protein: 351 AA.
 AC AAY23825;
 XX
 DT 15-SEP-1999 (first entry)
 XX
 DE A7 times membrane penetrating type receptor protein ET60.
 XX
 KM 7 times membrane-penetrating type receptor protein; ET60;
 KM leukocyte function; control; drug.
 XX
 OS Unidentified.
 XX
 OS JP1155573-A.
 XX
 PN 15-JUN-1999.
 PD

XX
 PF 27-NOV-1997; 97JP-0325823.
 XX
 PR 27-NOV-1997; 97JP-0325823.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI: 1999-398070/34.
 DR N-PSDB: AAX86032.
 XX
 PT New 7 times membrane-penetrating type receptor protein ET60 - useful
 PT for detecting drug controlling function of leukocyte
 XX
 PS Claim 1; Page 17-18; 20pp; Japanese.
 XX
 CC The present sequence represents a 7 times membrane-penetrating type
 CC receptor protein ET60. The 7 times membrane-penetrating type
 CC receptor protein ET60 can be used for detecting a drug controlling
 CC the function of leukocyte.
 CC
 SQ Sequence 351 AA;
 XX
 Query Match 74.2%; Score 1332; DB 20; Length 351;
 Best Local Similarity 75.2%; Pred. No. 7.5e-132;
 Matches 258; Conservative 36; Mismatches 47; Indels 2; Gaps 1;
 OY 2 AEHDYHEDYGFSSFNDS--OEHOEFLQFSKYVFLPCMYLVFVCGLVGNSLVVISIFY 59
 DB 9 ALYGHYEGDWLFRNNSDSEKRFLEKFEVFLPCYLVFVFGLVGNSLVVISIFY 68
 OY 60 HKLOSLDFVLNPLADLVFVCTLPFAVAGIHEWFGQVCKSLGITYINFTSMIL 119
 DB 69 OKLTLDFVLNPLADLVFVCTLPFAVAGIHEWFGQVCKSLGITYINFTSMIL 128
 OY 120 LTCITVDFRIYVVKATKAYNOQAKRMWGKVTSLIIVVSLVSLPQIITYGWVFNLDKIL 179
 DB 129 LTCITVDFRIYVVKATKAYNOQAKRMWGKVTSLIIVVSLVSLPQIITYGWVFNLDKIL 188
 OY 180 CGYHDEAISTVVLATQMTLGFELPLITMIVCYSVIIKTLHAGGFOKHSKLIIFLVMAVF 239
 DB 189 CGYHDEAISTVVLATQMTLGFELPLITMIVCYSVIIKTLHAGGFOKHSKLIIFLVMAVF 248
 OY 240 FLTQMPENLMKFIKSTHMEYYAMTSFHTITMTEALATLRACLNVPVLYAFVSLKFRKNF 299
 DB 249 FLTQMPENLMKFIKSTHMEYYAMTSFHTITMTEALATLRACLNVPVLYAFVSLKFRKNF 308
 OY 300 WKLVKDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 342
 DB 309 WKLVKDIGCLPYLGVSQWKSSEDNSKTPSASHNVEATSMFOL 351
 RESULT 15
 ID AAM70001
 XX AAM70001 standard; Protein: 302 AA.
 AC AAM70001;
 XX
 DT 20-OCT-1998 (first entry)
 XX
 DE Rodent chemokine receptor 94ID12 amino acid sequence.
 XX
 KM Chemokine; primate; human; rodent; chemokine receptor; asthma;
 KM inflammatory response; immune response; leukocyte migration; GPCR;
 KM leukocyte adhesion; chemotactant; modulation; antiviral response;
 KM cellular morphology modification response; G-protein coupled receptor;
 KM phospholipase 11b turnover; abnormal proliferation; regeneration;
 KM atrophy; 94ID12.
 XX
 OS Mus sp.
 XX
 OS WO9832858-A2.
 XX
 PN 30-JUL-1998.
 PD

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OM protein - protein search, using sw model

Run on: July 15, 2003, 07:20:41 ; Search time 53 Seconds

(without alignments)
751.237 Million cell updates/sec

Title: US-09-940-063-2

Perfect score: 1794

Sequence: 1 MAEHDYHEDYGFSSFNDSQ.....DNSKTFASHNVEATSMFOL 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 445758 seqs, 116419773 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/PCRUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1794	100.0	342	9	US-10-225-567A-348
2	1794	100.0	342	10	US-09-852-156-2
3	1794	100.0	342	10	US-09-940-063-2
4	1730	96.4	342	10	US-09-852-156-6
5	1717	95.7	342	10	US-09-852-156-4
6	617	34.4	374	9	US-10-225-567A-390
7	612	34.1	357	9	US-09-966-755-2
8	612	34.1	357	9	US-10-251-385-24
9	612	34.1	357	10	US-10-225-567A-241
10	612	34.1	357	10	US-09-903-377-2
11	612	34.1	357	10	US-09-952-385-2
12	612	34.1	357	12	US-10-000-759A-2
13	608.5	33.9	378	9	US-10-251-385-74
14	608.5	33.9	378	9	US-10-225-567A-68
15	606	33.8	357	9	US-10-251-385-176
16	604.5	33.7	378	9	US-10-251-385-204
17	568	31.7	350	9	US-09-968-433-79
18	560	31.2	349	10	US-09-765-994-4
19	560	31.2	350	9	US-09-968-433-16

20	560	31.2	350	9	US-10-282-837-8	Sequence 8, Appli
21	560	31.2	350	9	US-10-225-567A-607	Sequence 607, App
22	560	31.2	350	10	US-10-288-222A-10	Sequence 10, Appl
23	560	31.2	350	10	US-09-765-994-2	Sequence 2, Appli
24	560	31.2	350	10	US-09-796-338A-8	Sequence 8, Appli
25	527.5	29.4	360	10	US-09-938-719-7	Sequence 7, Appli
26	527.5	29.4	360	10	US-09-939-226-7	Sequence 7, Appli
27	527.5	29.4	360	10	US-09-938-703-7	Sequence 7, Appli
28	524.5	29.2	352	9	US-09-104-063-4	Sequence 4, Appli
29	524.5	29.2	352	9	US-10-225-567A-76	Sequence 76, Appli
30	524.5	29.2	352	9	US-10-245-850-1	Sequence 1, Appli
31	524.5	29.2	352	10	US-09-953-692-2	Sequence 2, Appli
32	524.5	29.2	352	10	US-09-953-717-2	Sequence 2, Appli
33	522.5	29.1	352	9	US-09-870-759-37	Sequence 37, Appli
34	522.5	29.1	352	9	US-09-870-759-144	Sequence 144, App
35	521.5	29.1	344	9	US-10-233-686-9	Sequence 9, Appli
36	521.5	29.1	344	9	US-10-067-800-9	Sequence 9, Appli
37	521.5	29.1	344	10	US-09-779-879A-9	Sequence 9, Appli
38	521.5	29.1	344	10	US-09-779-880A-9	Sequence 9, Appli
39	521.5	29.1	360	10	US-09-131-827A-20	Sequence 20, Appli
40	520.5	29.0	347	10	US-09-104-792-3	Sequence 3, Appli
41	520.5	29.0	360	9	US-10-225-567A-460	Sequence 460, App
42	520.5	29.0	360	10	US-09-131-827A-2	Sequence 2, Appli
43	512.5	28.6	355	9	US-10-225-567A-62	Sequence 62, Appli
44	512.5	28.6	355	9	US-10-245-850-2	Sequence 2, Appli
45	512.5	28.6	355	10	US-09-961-068-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1									
US-10-225-567A-348									
Sequence 348, Application US/10225567A									
Publication No. US20030113798A1									
GENERAL INFORMATION:									
APPLICANT: Lifespan Biosciences									
APPLICANT: Brown, Joseph P.									
APPLICANT: Burner, Glenn C.									
APPLICANT: Roush, Christine L.									
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR									
FILE REFERENCE: 1920-4-4									
CURRENT APPLICATION NUMBER: US/10/225,567A									
CURRENT FILING DATE: 2001-12-19									
PRIOR APPLICATION NUMBER: 60/257,144									
PRIOR FILING DATE: 2000-12-19									
NUMBER OF SEQ ID NOS: 2292									
SOFTWARE: PatentIn version 3.1									
SEQ ID NO 348									
LENGTH: 342									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-10-225-567A-348									
Query Match									
Best Local Similarity 100.0%; Score 1794; DB 9; Length 342;									
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MAEHDYHEDYGFSSFNDSQ	100.0%	9	US-10-225-567A-348	Sequence 348, App			
DB	1	MAEHDYHEDYGFSSFNDSQ	100.0%	9	US-10-225-567A-348	Sequence 348, App			
QY	61	KLOSITDVELNPLADLVFCTLPENYAGIHEHVEGOWCKSLGTYTINFTSMIL	100.0%	120	US-10-225-567A-348	Sequence 120, App			
DB	61	KLOSITDVELNPLADLVFCTLPENYAGIHEHVEGOWCKSLGTYTINFTSMIL	100.0%	120	US-10-225-567A-348	Sequence 120, App			
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DB	121	TCITVDREIVVVKATKAVNQAKRTWGTSLIWIISLVSPQIITGVNFNDKILC	100.0%	180	US-10-225-567A-348	Sequence 180, App			
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DB	181	GYNDEAISTVVLATQMTLGFPLPLITMIVCSVITIKTLHAGGQKHSKILIFLVAVF	100.0%	240	US-10-225-567A-348	Sequence 240, App			

OY 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
DB 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
OY 301 KLVADIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342
DB 301 KLVADIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342

RESULT 2

US-09-852-156-2
Sequence 2, Application US/09852156
Patent No. US20020076694A1

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.
Deng, Hongkui
Ramani, Vineet N.K.

Unutmaz, Derya

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS

ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/852,156

FILING DATE: 09-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: NO

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-852-156-2

Query Match 100.0%; Score 1794; DB 10; Length 342;

Best Local Similarity 100.0%; Pred. No. 9.8e-144;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAEHDYEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFCGLVNSLVYISIFYH 60
DB 1 MAEHDYEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFCGLVNSLVYISIFYH 60
OY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAVAGIHEWFGQVWCKSLGITYINFTSMIL 120
DB 61 KLSLTDVFLVNLPLADLVFVCTLPFWAVAGIHEWFGQVWCKSLGITYINFTSMIL 120

OY 121 TCITVDREIVVVKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIIYGVNPLDKLIC 180
DB 121 TCITVDREIVVVKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIIYGVNPLDKLIC 180
OY 181 GYHDEAISTVLAQMTLGFFLPITMIVCVSVIIKTLHAGGFOKHSKIIFLVAVF 240
DB 181 GYHDEAISTVLAQMTLGFFLPITMIVCVSVIIKTLHAGGFOKHSKIIFLVAVF 240
OY 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
DB 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
OY 301 KLVADIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342
DB 301 KLVADIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342

RESULT 3

US-09-940-063-2

Sequence 2, Application US/09940063

Patent No. US20020090657A1

GENERAL INFORMATION:

APPLICANT: Briskin, Michael J.

APPLICANT: Murphy, Kristine E.

APPLICANT: Wilbanks, Alyson M.

APPLICANT: Wu, Lijun

TITLE OF INVENTION: No. US20020090657A1el Antibodies and Ligands for "Bonzo"

FILE REFERENCE: 1855,1070-000

CURRENT APPLICATION NUMBER: US/09/940,063

PRIOR FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 09/449,437

NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 342

TYPE: PRT

ORGANISM: Homo sapiens

US-09-940-063-2

Query Match 100.0%; Score 1794; DB 10; Length 342;

Best Local Similarity 100.0%; Pred. No. 9.8e-144;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAEHDYEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFCGLVNSLVYISIFYH 60
DB 1 MAEHDYEDYGFSSFNDSOEHDPLQFSKVFPLPCMYLVVFCGLVNSLVYISIFYH 60
OY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAVAGIHEWFGQVWCKSLGITYINFTSMIL 120
DB 61 KLSLTDVFLVNLPLADLVFVCTLPFWAVAGIHEWFGQVWCKSLGITYINFTSMIL 120
OY 121 TCITVDREIVVVKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIIYGVNPLDKLIC 180
DB 121 TCITVDREIVVVKATKAYNOQAKRMWGKVTSLIWIISLVSLPQIIYGVNPLDKLIC 180
OY 181 GYHDEAISTVLAQMTLGFFLPITMIVCVSVIIKTLHAGGFOKHSKIIFLVAVF 240
DB 181 GYHDEAISTVLAQMTLGFFLPITMIVCVSVIIKTLHAGGFOKHSKIIFLVAVF 240
OY 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
DB 241 LITOMPENLMKFIKSTHWEYAMTSFHYTIVTEAIALRACLNPLVLAFAVSLKFRKNFW 300
OY 301 KLVADIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342
DB 301 KLVADIGCLPYLGVSHPKSSSEDSNKTFSASHNVEATSMFOL 342

RESULT 4

US-09-852-156-6

Sequence 6, Application US/09852156

Patent No. US20020076694A1
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Pigtail macaque
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
-09-852-156-6
Query Match 96.4%; Score 1730; DB 10; Length 342;
Best Local Similarity 95.6%; Pred. No. 2,5e-138;
Matches 327; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

1 MAEHYHEDYGFSSNDSSQEHODFLQFSKVFPLPCMYLVVFCGLVNSLVVISIYH 60
1 MAEHYHEDYGLNSFNSQEHODFLQFRVFLPCMYLVVFCGLVNSLVVISIYH 60
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKTLGTYTINFTSMIL 120
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKTLGTYTINFTSMIL 120
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKTLGTYTINFTSMIL 120
121 TCITVDRTIVVVKATKAYNOAKRMTGKVTSLTIWISLVSLPQIIYGVNFDKILC 180
121 TCITVDRTIVVVKATKAYNOAKRMTGKVTSLTIWISLVSLPQIIYGVNFDKILC 180
121 TCITVDRTIVVVKATKAYNOAKRMTGKVTSLTIWISLVSLPQIIYGVNFDKILC 180
181 GYHDEAISTVVALQMTLGFELPLMTIVCSVVIKTLHAAGFGOKHRSKTIIFLVMAVF 240
181 GYHDEAISTVVALQMTLGFELPLMTIVCSVVIKTLHAAGFGOKHRSKTIIFLVMAVF 240
181 GYHDEAISTVVALQMTLGFELPLMTIVCSVVIKTLHAAGFGOKHRSKTIIFLVMAVF 240
241 LITQPFMLVKIRISTHWEYAMTSFHTIWTETAIYLRACLNVLAFASIKRKNFW 300
241 LITQPFMLVKIRISTHWEYAMTSFHTIWTETAIYLRACLNVLAFASIKRKNFW 300
301 KLVKDIGCLPYLGVSHQKSSBDNSKTFPSASHNEATSMFOL 342

DB 301 KLVKDIGCLPYLGVSHQKSSBDNSKTFPSASHNEATSMFOL 342
RESULT 5
US-09-852-156-4
Sequence 4, Application US/09852156
Patent No. US20020076694A1
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/852,156
FILING DATE: 09-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: African Green Monkey
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
-09-852-156-4
Query Match 95.7%; Score 1717; DB 10; Length 342;
Best Local Similarity 95.3%; Pred. No. 3.1e-137;
Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

1 MAEHYHEDYGFSSNDSSQEHODFLQFSKVFPLPCMYLVVFCGLVNSLVVISIYH 60
1 MAEHYHEDYDNFNSQEHODFLQFSKVFPLPCMYLVVFCGLVNSLVVISIYH 60
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKTLGTYTINFTSMIL 120
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKTLGTYTINFTSMIL 120
61 KLOSLTDVFLNPLADLVFVCTLPFMAVAGIHEWFEQVWCKTLGTYTINFTSMIL 120
121 TCITVDRTIVVVKATKAYNOAKRMTGKVTSLTIWISLVSLPQIIYGVNFDKILC 180
121 TCITVDRTIVVVKATKAYNOAKRMTGKVTSLTIWISLVSLPQIIYGVNFDKILC 180
121 TCITVDRTIVVVKATKAYNOAKRMTGKVTSLTIWISLVSLPQIIYGVNFDKILC 180
181 GYHDEAISTVVALQMTLGFELPLMTIVCSVVIKTLHAAGFGOKHRSKTIIFLVMAVF 240
181 GYHDEAISTVVALQMTLGFELPLMTIVCSVVIKTLHAAGFGOKHRSKTIIFLVMAVF 240
181 GYHDEAISTVVALQMTLGFELPLMTIVCSVVIKTLHAAGFGOKHRSKTIIFLVMAVF 240

Db 181 GYHDEISTVVLATQMTLGFLLPLAMIVCVSIKILTLHAGGFOKHSKILIFLVAVF 240
QY 241 LITQMPENLMKFIKSTHWEYAMTSFHYITWTEAIAVLRAQLNPVLAFAVSLKFRKNFW 300
Db 241 LITQMPENLVKLKISTHWEYAMTSFHYITWTEAIAVLRAQLNPVLAFAVSLKFRKNFW 300
QY 301 KLIVDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 342
Db 301 KLIVDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 342
301 KLIVDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 342
RESULT 6
US-10-225-567A-390
Sequence 390, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
PRIORITY FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER OF SEQ ID NOS: 2392
SOFTWARE: PatentIn version 3.1
SEQ ID NO 390
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-390
Query Match 34.4%, Score 617, DB 9, Length 374;
Best Local Similarity 36.3%, Pred. No. 2e-44;
Matches 135, Conservative 77, Mismatches 116, Indels 44, Gaps 9;
QY 5 DYHEDYGFSSFNDSOEHODEL-----QSKVFLPCMYLVFVCGLVGNSLVAVIS 56
Db 13 DSSSDY-FVSVNTSYVSVDSEMLCSLOEVROFRLVPLVSLICVEGLGNILVITFE 71
QY 57 IFYHKLSLTPVFLVNLPLADLVFVCTLPFWAVA-GIHEWEGOVCKSLGITYTINPT 115
Db 72 AFYKASMTDVYILNMAIDILFVLDPFAVSHATGAWFSNATCKLKGITAINNC 131
QY 116 SMLITCTVDREFIVVVKATKAYNOQAKRMVGVTSLLIWLIVSLVSLPQIIYGNVNL 175
Db 132 GMLLTCTISMDRYIAIVQATKSFRLRSRTLPRTKIICLVWGLVITSSSFVENOKYNT 191
QY 176 D-KLIGCYHDEAIS-----TVLATOMTLGFLLPLAMIVCVSIKILTLHAGGFOKHR 228
Db 192 QGSVDCPEKQYQVSEPIRMKMLLGLLELFGFFLPMEMFCYFIVYKTLVQAOQNSRHK 251
QY 229 SLKTIIFVMAVFLITQMPENLM-----KFIKSTHWEYAMTSFHYITWTEAIAVL 279
Db 252 AIRITIAVVLVFLACQIPHNANVLLVTANLGNKMRSCOSE-----KLIGTYTIEVLAFL 307
QY 280 RACINPVLAFAVSLKFRKNFWKLVKDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 330
Db 308 HCCINPVLAFAVSLKFRKNFWKLVKDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 362
QY 331 SHNVEATSMFOL 342
Db 363 TADMDNASSFTM 374

APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
FILE REFERENCE: IKS98-16
CURRENT APPLICATION NUMBER: US/09/966,755
PRIORITY FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/266,464
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-966-755-2
Query Match 34.1%, Score 612, DB 9, Length 357;
Best Local Similarity 36.3%, Pred. No. 5.1e-44;
Matches 123, Conservative 82, Mismatches 100, Indels 34, Gaps 8;
QY 8 EDYGFSSFNDSOEHODEL-----LQSKVFLPCMYLVFVCGLVGNSLVAVIS 55
Db 3 DDYGFSSFNDSOEHODEL-----LQSKVFLPCMYLVFVCGLVGNSLVAVIS 60
QY 56 SIYHKLSLTPVFLVNLPLADLVFVCTLPFWAVA-GIHEWEGOVCKSLGITYTINPT 115
Db 61 YWYCTRVKTYTMDMLNLAIDILFVLDPFAVSHATGAWFSNATCKLKGITAINNC 120
QY 116 SMLITCTVDREFIVVVKATKAYNOQAKRMVGVTSLLIWLIVSLVSLPQIIYGNVNL 175
Db 121 CVLLIMCISVDRTAIAQAMRAHRTWRERLLYSMVCFTTWLAALCIPILISQIKEE 180
QY 176 DKL-ICGY---HDEA--ISVVLATQMTLGFLLPLAMIVCVSIKILTLHAGGFOKHS 229
Db 181 SGALICMIVPDSSTKLKSAVLKYLIGFLLPFWVMACCYITIIHTLQAKSSSKHA 240
QY 230 LKTIIFVMAVFLITQMPENLMKFIKSTHWEYAM-----TSFHYITWTEAIAVLRA 281
Db 241 LKTIIFVMAVFLITQMPENLMKFIKSTHWEYAM-----TSFHYITWTEAIAVLRA 298
QY 282 CLNPVLAFAVSLKFRKNFWKLVKDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 320
Db 299 CLNPVLAFAVSLKFRKNFWKLVKDIGCLPVLGVSQKSSSEDSKTSASHNVEATSMFOL 333
RESULT 8
US-10-251-385-24
Sequence 24, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Protein-Coupled
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
PRIORITY FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-251-385-24
Query Match 34.1%, Score 612, DB 9, Length 357;
Best Local Similarity 36.3%, Pred. No. 5.1e-44;
Matches 123, Conservative 82, Mismatches 100, Indels 34, Gaps 8;

```
OY      8 EDYGFSSFNDSOEHODE-----LOFSKYFLPCMYLVFVCGLVGNSLVLYI 55
      3 DDYG--SESTSMEDYVNFNTDFYCEKNVROFASHPLPLMYLVFVGLAGNSLVLY 60
DB
OY      56 SIFTHKQSLTDVFLVNLPLADLVFVCTLPFWATAAGHEWFGOVCKSLGITYNTYT 115
      61 YWCTRYKVTMTDMLNLAIADLFLVTLPLFWAIAADQMKFQFMCKVNSMKMNFYS 120
DB
OY      116 SMLITCTVDREFYVAVKATKAYNOAKRMVGTSLIIVISLVSLPOLIYGNVNL 175
      121 CVLLIMCISVDRTYIAQAMRAHTRERKRLYSKVCCTIIVLAALCIPILYSQIKEE 180
DB
OY      176 DKL-ICGY--HDEA--ISTVVLATQMTLGFELPLTMIVCYSVIITKLHAGGFQKHS 229
      181 SGAIACIMVYPSDESTKLSAVLLIKVLGFFLPVWACCTYIIHTLQAKKSSKHKA 240
DB
OY      230 LKIIFLVAVFLTLQMPENLMKFFIRSTHWEYAM-----TSFHTIMVTEAIVYRA 281
      241 LKVTITVTVFVLSQFPYNCILVOTI--DAYAMFISNCVSTNIDICFOYTQTIAPFHS 298
DB
OY      282 CLNPVLYAFVSLKFRKNFMKLVKIDICLPYLGVSQKMS 320
      299 CLNPVLYFVGERRRDLVKTLLKNGCIS---QAQWVS 333
DB
```

RESULT 9

```
US-10-225-567A-241
; Sequence 241, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
10-225-567A-241
```

```
Query Match      34.1%; Score 612; DB 9; Length 357;
Best Local Similarity 36.3%; Pred. No. 5,1e-44;
Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;
```

```
OY      8 EDYGFSSFNDSOEHODE-----LOFSKYFLPCMYLVFVCGLVGNSLVLYI 55
      3 DDYG--SESTSMEDYVNFNTDFYCEKNVROFASHPLPLMYLVFVGLAGNSLVLY 60
DB
OY      56 SIFTHKQSLTDVFLVNLPLADLVFVCTLPFWATAAGHEWFGOVCKSLGITYNTYT 115
      61 YWCTRYKVTMTDMLNLAIADLFLVTLPLFWAIAADQMKFQFMCKVNSMKMNFYS 120
DB
OY      116 SMLITCTVDREFYVAVKATKAYNOAKRMVGTSLIIVISLVSLPOLIYGNVNL 175
      121 CVLLIMCISVDRTYIAQAMRAHTRERKRLYSKVCCTIIVLAALCIPILYSQIKEE 180
DB
OY      176 DKL-ICGY--HDEA--ISTVVLATQMTLGFELPLTMIVCYSVIITKLHAGGFQKHS 229
      181 SGAIACIMVYPSDESTKLSAVLLIKVLGFFLPVWACCTYIIHTLQAKKSSKHKA 240
DB
OY      230 LKIIFLVAVFLTLQMPENLMKFFIRSTHWEYAM-----TSFHTIMVTEAIVYRA 281
      241 LKVTITVTVFVLSQFPYNCILVOTI--DAYAMFISNCVSTNIDICFOYTQTIAPFHS 298
DB
```

```
OY      282 CLNPVLYAFVSLKFRKNFMKLVKIDICLPYLGVSQKMS 320
      299 CLNPVLYFVGERRRDLVKTLLKNGCIS---QAQWVS 333
DB
```

RESULT 10

```
US-09-903-377-2
; Sequence 2, Application US/09903377
; Patent No. US20020116727A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
; FILE REFERENCE: R-365
; CURRENT APPLICATION NUMBER: US/09/903,377
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/217,255
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/221,483
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/262,113
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting vector
US-09-903-377-2
```

```
Query Match      34.1%; Score 612; DB 10; Length 357;
Best Local Similarity 36.3%; Pred. No. 5,1e-44;
Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;
```

```
OY      8 EDYGFSSFNDSOEHODE-----LOFSKYFLPCMYLVFVCGLVGNSLVLYI 55
      3 DDYG--SESTSMEDYVNFNTDFYCEKNVROFASHPLPLMYLVFVGLAGNSLVLY 60
DB
OY      56 SIFTHKQSLTDVFLVNLPLADLVFVCTLPFWATAAGHEWFGOVCKSLGITYNTYT 115
      61 YWCTRYKVTMTDMLNLAIADLFLVTLPLFWAIAADQMKFQFMCKVNSMKMNFYS 120
DB
OY      116 SMLITCTVDREFYVAVKATKAYNOAKRMVGTSLIIVISLVSLPOLIYGNVNL 175
      121 CVLLIMCISVDRTYIAQAMRAHTRERKRLYSKVCCTIIVLAALCIPILYSQIKEE 180
DB
OY      176 DKL-ICGY--HDEA--ISTVVLATQMTLGFELPLTMIVCYSVIITKLHAGGFQKHS 229
      181 SGAIACIMVYPSDESTKLSAVLLIKVLGFFLPVWACCTYIIHTLQAKKSSKHKA 240
DB
OY      230 LKIIFLVAVFLTLQMPENLMKFFIRSTHWEYAM-----TSFHTIMVTEAIVYRA 281
      241 LKVTITVTVFVLSQFPYNCILVOTI--DAYAMFISNCVSTNIDICFOYTQTIAPFHS 298
DB
OY      282 CLNPVLYAFVSLKFRKNFMKLVKIDICLPYLGVSQKMS 320
      299 CLNPVLYFVGERRRDLVKTLLKNGCIS---QAQWVS 333
DB
```

RESULT 11

```
US-09-952-385-2
; Sequence 2, Application US/09952385
; Patent No. US20020119504A1
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
; FILE REFERENCE: LWS98-16
; CURRENT APPLICATION NUMBER: US/09/952,385
```

CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows version 3.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-952-385-2

Query Match 34.1%; Score 612; DB 10; Length 357;
Best Local Similarity 36.3%; Pred. No. 5,1e-44;
Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;

QY 8 EDYGFSSFNDSQOEHOE-----LQFSKVFPCMYLVFVCGLVGNSLVYI 55
DB 3 DDYG--SESTSSMEDYVNFNFTDFCEKNNVROFASHFLPPLVYLVFVGLGNSLVYI 60
QY 56 SIEFHKLQSLDVLVNLPLADLVFVCTLPFWAYAGHEWFGVGMCKSLGITYINFT 115
DB 61 YWCTRVKTMDFMLNLAIADLLFLVTLPEWALAAADQMFQTFMCKVNSMYKMEYS 120
QY 116 SMLITCTVDFRIFYVATKAYNOQAKRMGKVTSLIIVISLVSIPQIIGNVENL 175
DB 121 CVLLIMCISVDRYIAIQAMAHHTWRERKRLYSKMVCTIIVLAALCIPILISQKEE 180
QY 176 DKL-ICGY--HDEA--ISTVLATQMTLGFELPLTMIVCYSVIIRKLHAGFQKHS 229
DB 181 SGAIICMVVPSDESTKLSAVLTKVLGFEFLPFVMACCYTIIHILIOAKSSKHA 240
QY 230 LKIFILVAVFLLTQMPENLKFIRSTHWEYAM-----TSFHTIIVTEAIVARA 281
DB 241 LKVTITVLVAVLSQFPNCLILVQTI--DAYAMFISNCVSTINDICFOVTQTIAPFHS 298
QY 282 CLNPVLVAFVSLKFRKNFWKLVKDIGCLPYLGVSQKHS 320
DB 299 CLNPVLVAFVGERFRRLDVKTKNLGCTIS---QAQWVS 333

RESULT 12
US-10-000-759A-2
Sequence 2, Application US/10000759A
Patent No. US20020141991A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING MODULATORS OF GPR-9-6 FUNCTION
FILE REFERENCE: 1855, 1064-003
CURRENT APPLICATION NUMBER: US/10/000,759A
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US/09/522,752
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: US 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-000-759A-2

Query Match 34.1%; Score 612; DB 12; Length 357;
Best Local Similarity 36.3%; Pred. No. 5,1e-44;
Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;

QY 8 EDYGFSSFNDSQOEHOE-----LQFSKVFPCMYLVFVCGLVGNSLVYI 55
DB 3 DDYG--SESTSSMEDYVNFNFTDFCEKNNVROFASHFLPPLVYLVFVGLGNSLVYI 60

QY 56 SIEFHKLQSLDVLVNLPLADLVFVCTLPFWAYAGHEWFGVGMCKSLGITYINFT 115
DB 61 YWCTRVKTMDFMLNLAIADLLFLVTLPEWALAAADQMFQTFMCKVNSMYKMEYS 120
QY 116 SMLITCTVDFRIFYVATKAYNOQAKRMGKVTSLIIVISLVSIPQIIGNVENL 175
DB 121 CVLLIMCISVDRYIAIQAMAHHTWRERKRLYSKMVCTIIVLAALCIPILISQKEE 180
QY 176 DKL-ICGY--HDEA--ISTVLATQMTLGFELPLTMIVCYSVIIRKLHAGFQKHS 229
DB 181 SGAIICMVVPSDESTKLSAVLTKVLGFEFLPFVMACCYTIIHILIOAKSSKHA 240
QY 230 LKIFILVAVFLLTQMPENLKFIRSTHWEYAM-----TSFHTIIVTEAIVARA 281
DB 241 LKVTITVLVAVLSQFPNCLILVQTI--DAYAMFISNCVSTINDICFOVTQTIAPFHS 298
QY 282 CLNPVLVAFVSLKFRKNFWKLVKDIGCLPYLGVSQKHS 320
DB 299 CLNPVLVAFVGERFRRLDVKTKNLGCTIS---QAQWVS 333

RESULT 13
US-10-251-385-74
Sequence 74, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-251-385-74

Query Match 33.9%; Score 608.5; DB 9; Length 378;
Best Local Similarity 36.9%; Pred. No. 1,1e-43;
Matches 122; Conservative 84; Mismatches 106; Indels 19; Gaps 8;

QY 24 QDFLQFSKVFLLPCMYLVFVCGLVGNSLVYISIFYHKLQSLDVLVNLPLADLVFVCT 83
DB 51 KDVANFRKAMFLPIMYSILICEVGLGNGLVVLYTFERKLTMDTYLLNLAVADILFLT 110
QY 84 LPEFAYAGHEWFGVGMCKSLGITYINFTSMILITCTVDFRIFYVATKAYNOQAK 143
DB 111 LPEFAYAAKSWPFGVHFCILIPATYMSFSGMLLCTSIDRYAIVQAVSAHRRAR 170
QY 144 RMTWGVTSLLIIVISLVSIPQIIGNV---FNLDKLICGY--HDEAISTVLATQMT 197
DB 171 VLLISKLSVGIWILATVLSIPELYSIDLQSSSEQAMRSLTHEVEAFITQVA-QWY 229
QY 198 LGFFPLPLTMIVCYSVIIRKLHAGFQKHSKIIFLVAVVAVLTLQMPEN-----LM 250
DB 230 IGFVLPLLAASFVLYIIRTLQARNERKRAKIVIAVVAVFIVPOLPYNGVLAQYVA 289
QY 251 KF-IRSTHWEYAMTSFHTIIVTEAIVARACTNPVLVAFVSLKFRKNFWKLVKDIGCL 309
DB 290 NFNITSTGCLSQOLNIAID--VYISLACYRCVNPFLAIGVKKFRNDLFKFLKDLGL 347
QY 310 PYLGVSQKHSSEDSNKTFSASHNVEATSNF 340
DB 348 SQEQL-RQWSSCR-HIRRSMSVEAEITTTTF 376

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 07:17:25 ; Search time 26 Seconds
(Without alignments)
387.025 Million cell updates/sec

Title: US-09-940-063-2

Perfect score: 1794
Sequence: 1 MAEDHYHEDGFSSFNDSQ.....DNKTFESASHNEATSMFOL 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Indexed: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1794	100.0	342	2	US-08-742-011-2
2	1794	100.0	342	4	US-09-275-384B-5
3	1794	100.0	342	4	US-09-116-498-2
4	1794	100.0	342	4	US-09-449-437A-2
5	1794	100.0	342	4	US-09-517-605-9
6	1730	96.4	342	4	US-09-116-498-6
7	1717	95.7	342	4	US-09-116-498-4
8	619	34.5	374	4	US-09-045-583-48
9	619	34.5	374	4	US-09-534-185-48
10	612	34.1	357	4	US-09-266-464-2
11	608.5	33.9	358	1	US-08-153-848-19
12	608.5	33.9	358	3	US-09-299-843A-19
13	608.5	33.9	358	4	US-09-088-337B-19
14	608.5	33.9	358	5	PCT-US93-11153-19
15	608.5	33.9	378	1	US-08-153-848-15
16	608.5	33.9	378	3	US-09-299-843A-15
17	608.5	33.9	378	3	US-09-299-843A-66
18	608.5	33.9	378	4	US-09-251-545-1
19	608.5	33.9	378	4	US-09-088-337B-15
20	608.5	33.9	378	4	US-09-088-337B-66
21	608.5	33.9	378	5	PCT-US93-11153-15
22	608.5	33.9	410	1	US-08-153-848-7
23	608.5	33.9	410	3	US-09-299-843A-7
24	608.5	33.9	410	3	US-09-088-337B-7
25	608.5	33.9	410	5	PCT-US93-11153-7
26	606	33.8	359	1	US-08-153-848-24
27	606	33.8	359	3	US-09-299-843A-24

28	606	33.8	359	4	US-09-088-337B-24	Sequence 24, Appl
29	606	33.8	359	5	PCT-US93-11153-24	Sequence 24, Appl
30	588.5	32.8	378	1	US-08-383-750-2	Sequence 2, Appl
31	588.5	32.8	378	1	US-08-383-751A-2	Sequence 2, Appl
32	588.5	32.8	378	4	US-08-352-678-2	Sequence 2, Appl
33	588.5	32.8	378	4	US-09-045-583-49	Sequence 49, Appl
34	588.5	32.8	378	5	PCT-US93-09636-2	Sequence 2, Appl
35	588.5	32.8	378	5	PCT-US93-09636-2	Sequence 49, Appl
36	568	31.7	350	2	US-08-966-316-18	Sequence 18, Appl
37	560	31.2	350	2	US-08-966-316-16	Sequence 16, Appl
38	554	30.9	361	2	US-08-902-294-2	Sequence 2, Appl
39	554	30.9	361	3	US-09-178-637-2	Sequence 2, Appl
40	527.5	29.4	360	4	US-08-833-752-7	Sequence 7, Appl
41	524.5	29.2	352	1	US-08-202-056-3	Sequence 3, Appl
42	524.5	29.2	352	1	US-08-076-093A-4	Sequence 4, Appl
43	524.5	29.2	352	1	US-08-701-265-4	Sequence 4, Appl
44	524.5	29.2	352	1	US-08-284-586-4	Sequence 4, Appl
45	524.5	29.2	352	2	US-08-805-478-4	Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-08-742-011-2
: Sequence 2, Application US/08742011
: Patent No. 5824504
:
GENERAL INFORMATION:
: APPLICANT: Elshourbagy, Nabil A.
: APPLICANT: Bergsma, Dirk J.
: APPLICANT: Ellis, Catherine E.
: TITLE OF INVENTION: Human 7-Transmembrane Receptor
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESS: Smithline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19406-2799
:
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
:
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/742,011
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Han, William T.
: REGISTRATION NUMBER: 34,344
: REFERENCE/DOCKET NUMBER: ATG50020P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-5090
: TELEFAX: 610-270-5219
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 342 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-08-742-011-2
:
Query Match      100.0%; Score 1794; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
QY      1 MAEDHYHEDGFSSFNDSQDEHODFLQFSKVPICMYLVVFCGLGNSLVITSTFYH 60
:      |||
DB      1 MAEDHYHEDGFSSFNDSQDEHODFLQFSKVPICMYLVVFCGLGNSLVITSTFYH 60
:      |||
QY      61 KLSLTDVFLVNLPLADLVFVCTLPFWAYAGIHBEWFGQWCKSLGITYINFTSMIL 120
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Db 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWFGVOMKSLGIIITINFTSMIL 120
QY 121 TCITVDRFIVVAKATKAYNOAKRMWGVISLLIWIISLVSLPQIITGVNPNLKLIC 180
Db 121 TCITVDRFIVVAKATKAYNOAKRMWGVISLLIWIISLVSLPQIITGVNPNLKLIC 180
QY 181 GYHDEAISTVVLATOMTIGFELPLIMIVCYSVIITKLHAGGFORHRSKIIIFLVMAVF 240
Db 181 GYHDEAISTVVLATOMTIGFELPLIMIVCYSVIITKLHAGGFORHRSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIIRSTHMEYYAMTSFHYTIMVTEAIALRACINPVLVYAFVSLKFRKNFW 300
Db 241 LITOMPENLMKFIIRSTHMEYYAMTSFHYTIMVTEAIALRACINPVLVYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342

RESULT 2
US-09-275-384B-5
Sequence 5, Application US/09275384B
Patent No. 6232084
GENERAL INFORMATION:
APPLICANT: MACPHEE, COLIN HOUSTON
APPLICANT: MOORES, KITTY
TITLE OF INVENTION: NEW USE
FILE REFERENCE: GH-31106
CURRENT APPLICATION NUMBER: US/09/275.384B
CURRENT FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 9806677.2
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 342
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-275-384B-5

Query Match 100.0%; Score 1794; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEHDYHEDYGFSSFNDSOEHOEODFLOFSKVFELPCMYLVFVCGLVGNSLVYISIFHY 60
Db 1 MAEHDYHEDYGFSSFNDSOEHOEODFLOFSKVFELPCMYLVFVCGLVGNSLVYISIFHY 60
QY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWFGVOMKSLGIIITINFTSMIL 120
Db 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWFGVOMKSLGIIITINFTSMIL 120
QY 121 TCITVDRFIVVAKATKAYNOAKRMWGVISLLIWIISLVSLPQIITGVNPNLKLIC 180
Db 121 TCITVDRFIVVAKATKAYNOAKRMWGVISLLIWIISLVSLPQIITGVNPNLKLIC 180
QY 181 GYHDEAISTVVLATOMTIGFELPLIMIVCYSVIITKLHAGGFORHRSKIIIFLVMAVF 240
Db 181 GYHDEAISTVVLATOMTIGFELPLIMIVCYSVIITKLHAGGFORHRSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIIRSTHMEYYAMTSFHYTIMVTEAIALRACINPVLVYAFVSLKFRKNFW 300
Db 241 LITOMPENLMKFIIRSTHMEYYAMTSFHYTIMVTEAIALRACINPVLVYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342

RESULT 3
US-09-116-498-2
Sequence 2, Application US/09116498

Patent No. 6251582
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116.498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-116-498-2

Query Match 100.0%; Score 1794; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEHDYHEDYGFSSFNDSOEHOEODFLOFSKVFELPCMYLVFVCGLVGNSLVYISIFHY 60
Db 1 MAEHDYHEDYGFSSFNDSOEHOEODFLOFSKVFELPCMYLVFVCGLVGNSLVYISIFHY 60
QY 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWFGVOMKSLGIIITINFTSMIL 120
Db 61 KLSLTDVFLVNLPLADLVFVCTLPFWAAGIHEWFGVOMKSLGIIITINFTSMIL 120
QY 121 TCITVDRFIVVAKATKAYNOAKRMWGVISLLIWIISLVSLPQIITGVNPNLKLIC 180
Db 121 TCITVDRFIVVAKATKAYNOAKRMWGVISLLIWIISLVSLPQIITGVNPNLKLIC 180
QY 181 GYHDEAISTVVLATOMTIGFELPLIMIVCYSVIITKLHAGGFORHRSKIIIFLVMAVF 240
Db 181 GYHDEAISTVVLATOMTIGFELPLIMIVCYSVIITKLHAGGFORHRSKIIIFLVMAVF 240
QY 241 LITOMPENLMKFIIRSTHMEYYAMTSFHYTIMVTEAIALRACINPVLVYAFVSLKFRKNFW 300
Db 241 LITOMPENLMKFIIRSTHMEYYAMTSFHYTIMVTEAIALRACINPVLVYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHQWKSSEDNSKTFSSASHNEATSMFOL 342

Db 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342

RESULT 4
US-09-449-437A-2
Sequence 2, Application US/09449437A

Patent No. 6319675
GENERAL INFORMATION:
APPLICANT: Briskin, Michael J.
APPLICANT: Murphy, Kristine E.
APPLICANT: Wu, Lijun
APPLICANT: Alibanks, Alyson M.
TITLE OF INVENTION: No. 6319675el Antibodies and Ligands for "Bonzo"
TITLE OF INVENTION: Chemokine Receptor
FILE REFERENCE: 1855.1070-000
CURRENT APPLICATION NUMBER: US/09/449,437A
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-09-449-437A-2

Query Match 100.0%; Score 1794; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHYEDYGFSSFNDSOEEDFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
Db 1 MAEHYEDYGFSSFNDSOEEDFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
QY 61 KLGSLTDFVLNPLADLVFCTLPFAYAGIHFWGVQWCKSLGIYTFNFTSMIL 120
Db 61 KLGSLTDFVLNPLADLVFCTLPFAYAGIHFWGVQWCKSLGIYTFNFTSMIL 120
QY 121 TCITVDFIYVVKATKAYNOQAKRMWGKVTSLIWIISLVSPQIYYGVNFDKILIC 180
Db 121 TCITVDFIYVVKATKAYNOQAKRMWGKVTSLIWIISLVSPQIYYGVNFDKILIC 180
QY 181 GYHDEAISTVAVLATQMTLGFPLPLTMIVCVSVIITKLHAGFQKHRSKLIIFLVAVF 240
Db 181 GYHDEAISTVAVLATQMTLGFPLPLTMIVCVSVIITKLHAGFQKHRSKLIIFLVAVF 240
QY 241 LITQMPFNLMKFIRSTHWEYAMTSFHTITWTEAIAVLRACLPVLYAFVSLKFRKNFW 300
Db 241 LITQMPFNLMKFIRSTHWEYAMTSFHTITWTEAIAVLRACLPVLYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342

RESULT 5
US-09-517-605-9
Sequence 9, Application US/09517605
Patent No. 6319675
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: Geiltenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 342

TYPE: PRT
ORGANISM: Homo sapiens
US-09-517-605-9

Query Match 100.0%; Score 1794; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEHYEDYGFSSFNDSOEEDFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
Db 1 MAEHYEDYGFSSFNDSOEEDFLOFSKVFPLPCMYLVFVCGVGNLSLVISIFYH 60
QY 61 KLGSLTDFVLNPLADLVFCTLPFAYAGIHFWGVQWCKSLGIYTFNFTSMIL 120
Db 61 KLGSLTDFVLNPLADLVFCTLPFAYAGIHFWGVQWCKSLGIYTFNFTSMIL 120
QY 121 TCITVDFIYVVKATKAYNOQAKRMWGKVTSLIWIISLVSPQIYYGVNFDKILIC 180
Db 121 TCITVDFIYVVKATKAYNOQAKRMWGKVTSLIWIISLVSPQIYYGVNFDKILIC 180
QY 181 GYHDEAISTVAVLATQMTLGFPLPLTMIVCVSVIITKLHAGFQKHRSKLIIFLVAVF 240
Db 181 GYHDEAISTVAVLATQMTLGFPLPLTMIVCVSVIITKLHAGFQKHRSKLIIFLVAVF 240
QY 241 LITQMPFNLMKFIRSTHWEYAMTSFHTITWTEAIAVLRACLPVLYAFVSLKFRKNFW 300
Db 241 LITQMPFNLMKFIRSTHWEYAMTSFHTITWTEAIAVLRACLPVLYAFVSLKFRKNFW 300
QY 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342
Db 301 KLVKDIGCLPYLGVSHPKSSSEDSKTFSSASHNEATSMFOL 342

RESULT 6
US-09-116-498-6
Sequence 6, Application US/09116498
Patent No. 6251582

GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramanil, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USE
THEREOF

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: pigtail macaque
SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-09-116-498-6

Query Match 96.4%; Score 1730; DB 4; Length 342;
Best Local Similarity 95.6%; Pred. No. 3.6e-137;
Matches 327; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

1 MAEHDYHEDYGFSSFNDSOEHDPLQFSKVPFLPCMYLVVFGVGLVNSLVVLSIFH 60
1 MAEHDYHEDYGLNFSNDSOEHDPLQFSKVPFLPCMYLVVFGVGLVNSLVVLSIFH 60
61 KLOSITDVFVNLPLADLVFVCTLPFWAAGIHFWGVGWCKSLGITYINFTSMIL 120
61 KLOSITDVFVNLPLADLVFVCTLPFWAAGIHFWGVGWCKSLGITYINFTSMIL 120
121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIIYGVNFDKILC 180
121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIIYGVNFDKILC 180
121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIIYGVNFDKILC 180
181 GYHDEASTVLAQTMLGFFLLIMVICYSVIITKTLHAGGQKRSKIIIFLVAVF 240
181 GYHDEASTVLAQTMLGFFLLIMVICYSVIITKTLHAGGQKRSKIIIFLVAVF 240
181 GYHDEASTVLAQTMLGFFLLIMVICYSVIITKTLHAGGQKRSKIIIFLVAVF 240
241 LTQMPFNLMKFRSTHWEYAMTSFHYITMTVAIAYLRACLPVLYAVSLKFRNF 300
241 LTQMPFNLMKFRSTHWEYAMTSFHYITMTVAIAYLRACLPVLYAVSLKFRNF 300
241 LTQMPFNLMKFRSTHWEYAMTSFHYITMTVAIAYLRACLPVLYAVSLKFRNF 300
301 KLVNDIGCLPYLGSHOMKSEDSKTFSSASHNEATSMFOL 342
301 KLVNDIGCLPYLGSHOMKSEDSKTFSSASHNEATSMFOL 342

RESULT 7
US-09-116-498-4
Sequence 4, Application US/09116498
Patent No. 6251582
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: African Green Monkey
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-116-498-4

Query Match 95.7%; Score 1717; DB 4; Length 342;
Best Local Similarity 95.3%; Pred. No. 4.4e-136;
Matches 326; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

1 MAEHDYHEDYGFSSFNDSOEHDPLQFSKVPFLPCMYLVVFGVGLVNSLVVLSIFH 60
1 MAEHDYHEDYGLNFSNDSOEHDPLQFSKVPFLPCMYLVVFGVGLVNSLVVLSIFH 60
61 KLOSITDVFVNLPLADLVFVCTLPFWAAGIHFWGVGWCKSLGITYINFTSMIL 120
61 KLOSITDVFVNLPLADLVFVCTLPFWAAGIHFWGVGWCKSLGITYINFTSMIL 120
121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIIYGVNFDKILC 180
121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIIYGVNFDKILC 180
121 TCITVDREFIVVVKATKAYNOAKRMWGKYSLLIWIISLVSLPQIIYGVNFDKILC 180
181 GYHDEASTVLAQTMLGFFLLIMVICYSVIITKTLHAGGQKRSKIIIFLVAVF 240
181 GYHDEASTVLAQTMLGFFLLIMVICYSVIITKTLHAGGQKRSKIIIFLVAVF 240
181 GYHDEASTVLAQTMLGFFLLIMVICYSVIITKTLHAGGQKRSKIIIFLVAVF 240
241 LTQMPFNLMKFRSTHWEYAMTSFHYITMTVAIAYLRACLPVLYAVSLKFRNF 300
241 LTQMPFNLMKFRSTHWEYAMTSFHYITMTVAIAYLRACLPVLYAVSLKFRNF 300
241 LTQMPFNLMKFRSTHWEYAMTSFHYITMTVAIAYLRACLPVLYAVSLKFRNF 300
301 KLVNDIGCLPYLGSHOMKSEDSKTFSSASHNEATSMFOL 342
301 KLVNDIGCLPYLGSHOMKSEDSKTFSSASHNEATSMFOL 342

RESULT 8
US-09-045-583-48
Sequence 48, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: NO. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; LENGTH: 357
; TYPE: PRT
;

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ORGANISM: Homo sapiens
US-09-266-464-2

Query Match 34.1%; Score 612; DB 4; Length 357;
Best Local Similarity 36.3%; Pred. No. 8e-44;

Matches 123; Conservative 82; Mismatches 100; Indels 34; Gaps 8;

QY 8 EDYGFSSFNDSQGEHQDF-----LQFSKVELPCMLVYFVCGLSVSLVLT 55
DB 3 DDYG--SESTSMEDYVNFNFETDCECKNNVROFASHFLPPLVWLVFVIGALNSVLT 60
QY 56 SIYHKLQSLDVLVNLPLADLVFVCTLPFVAVAGCHEWVFGQWCKSLGITYTNEY 115
DB 61 YWCTRKMTDMLNLADLPLVTLPEFMAIADQKFEQTECKVNSWKNMYS 120
QY 116 SMLICIFVDFRIVVVKATKAYNOQAKRMWGKVTSLIIVISLVSLPOLIYGNVNL 175
DB 121 CVLLINCISVDRIATAQAMRAHTWREKRLYSKMCFTIIVLAALCPEILYSQKEE 180
QY 176 DKL-ICGY--HDEA--ISTVLAOTMTLGEFPLPLMTVYCVIIKTLHAGGFQKHS 229
DB 181 SGIAICTMVPSESTFKLSAVLTLKYLGLFPLFVVMACCTYIIHTLIQAKKSKKA 240
QY 230 LKTIPLVMAVELLTQMPENMKRIRSTHMEYAM-----TSFHTIVTEALVLA 261
DB 241 LKTIIVLVFVLSQEPYNCILVQTL--DAYAMFISNCVSTINDICFOVOTIAFHS 298
QY 282 CLNPVLYAFVSLKFRKNFVLKIDICLPYLGVSQWKS 320
DB 299 CLNPVLYFVGERFRDLYTKLNLGICIS----QAQWVS 333

RESULT 11
US-08-153-848-19

Sequence 19, Application US/08153848

Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schwellart, Vicki L.

TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,848

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5759804and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 358 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-19

Query Match 33.9%; Score 608.5; DB 1; Length 358;
Best Local Similarity 36.9%; Pred. No. 1.6e-43;

Matches 122; Conservative 84; Mismatches 106; Indels 19; Gaps 8;

QY 24 QDFLOFSKVELPCMLVYFVCGLSVSLVLTIFPCHKQSLDVLVNLPLADLVFVCT 83
DB 31 KDVNRKAMFLPMTYSITCEVGLGNGLVLTITFRRLKTMIDTYLLNLAADILFLT 90
QY 84 LPEWAVAGCHEWVFGQWCKSLGITYTNEYSMILFCTIVDFRIVVVKATKAYNOQAK 143
DB 91 LPEWAVSAKSWVGFVHFCKLIFAIYKMSFSGMLLLICISIDRYAVAIQVSAHRRAR 150
QY 144 RMTWGVTSLLIIVISLVSLPOLIYGNV---ENLKLICGY--HDEAISTVLAOTMT 197
DB 151 VLLISKLSCVGIWLTAVLSIPELVSDLQSSSEQAMRCSLTTEHVEAETITQVA-QWV 209
QY 198 LGFPLPLMTVYCVSYIKTLHAGGFQKHSKTIIFVWVAVFLTQMPEN-----LM 250
DB 210 IGFVLPLAMSFCYVLIIRLLQARFERRKAKVIAVYVETVQPLNGVLAQYA 269
QY 251 KF-IRSTHMEYAMTSFHTIVTEALVLAQCLNPVLYAFVSLKFRKNFVLKIDICL 309
DB 270 NFNTSSTCLSKQLNLAVD--VTYSLACVRCVNPFLVAFIVKFRNDLFKLEKIDICL 327
QY 310 PYLGVSQWKSSEDNSKTFESASHNVENTSMF 340
DB 328 SQEOL-RQWSSCR-HIRSSMSVEAEFTTTF 356

RESULT 12
US-09-299-843A-19

Sequence 19, Application US/09299843A

Patent No. 6107475

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schwellart, Vicki L.

TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/299,843A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/088,337

FILING DATE: 01-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848

FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: JILL E. DHI

REGISTRATION NUMBER: 43,213

